



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

*In re* Application of: )  
ZHELNIN and BLOOMQUIST ) Group Art Unit: 1645  
Serial No. 09/899,532 ) Examiner: S. Gucker  
Filing Date: July 6, 2001 ) Docket No. 02973.00040

For: **HUMAN NEUROPEPTIDE Y-LIKE G PROTEIN-COUPLED RECEPTOR**

**DECLARATION UNDER 37 C.F.R. § 1.131**

U.S. Patent and Trademark Office  
220 20th Street S.  
Customer Window, Mail Stop AF  
Crystal Plaza Two, Lobby, Room 1B03  
Arlington, VA 22202

Dear Sir:

We, Leonid Zhelnin and Brian Bloomquist, declare as follows:

1. We are the named inventors of the subject matter claimed in the application referenced above.
2. Prior to March 2, 2000, we reduced to practice the subject matter of claims 1-8 and 12 of the application referenced above. The dates on the attached exhibits have been redacted; however, all the work described in this declaration was performed in the United States prior to March 2, 2000.
3. Prior to March 2, 2000, we searched for sequences that could be used to clone novel GPCRs with homology to orexin-2 and NPY1 receptors. We identified these sequences by

BEST AVAILABLE COPY

monitoring search results from a program (Gene Agent) that automatically checks sequences released into the public domain for homology to the orexin-2 and NPY1 receptors.

4. Prior to March 2, 2000, we received reports from both the Gene Agent program orexin-2 and NPY1 receptor searches indicating that DNAs within accession numbers EM:AC005961.1 (Homo sapiens Chromosome 11q12.2 PAC pDJ32L16 genomic DNA) and GB:g3823006 (Human sperm genomic library; Accession number AQ270411) each had homology to orexin-2 and NPY1 receptor sequences. Copies of the reports are attached as Exhibits 1 and 2.

5. Exhibit 1 identifies G3823006 as having homology to the orexin-2 receptor sequence. Pages 1 through 3 of Exhibit 1 contain analysis results from the search for sequences with homology to the orexin-2 receptor. See the top of page 1, which describes the "Project Name" as "orexin receptor homology search." In the "Protein Agent" box near the bottom of page 1, the location of G3823006 ("GB:g3823006") relative to the orexin-2 receptor sequence (OX2R) is shown. Pages 2 and 3 of Exhibit 1 contain initial information about G3823006 (beginning with the last set of boxes on page 2). Pages 4 and 5 of Exhibit 1 provide more detailed information on G3823006, including its length of 483 nucleotides.

6. Exhibit 2 identifies AC005961 as having homology to the orexin-2 receptor sequence. Pages 1 and 2 of Exhibit 2 also contain analysis results from the search for sequences with homology to the orexin-2 receptor. See the top of page 1, which describes the "Project Name" as "orexin receptor homology search." Page 2 of Exhibit 2 specifically contains information about AC005961 (last set of boxes on page 2). Page 3 of Exhibit 2 contains a summary of the search results for sequences with homology to the orexin-2 receptor. See the top of page 3, which indicates that the "Project Name" is "orexin receptor homology search." The

middle portion of page 3 (“Sequences”) contains a short description of each of the seven sequences identified by the search. These sequences include both accession numbers EM:AC005961 and GB:g3823006. Page 4 of Exhibit 1 provides additional information about accession number AC005961.1, including its length of 154,647 nucleotides.

7. We analyzed the sequences of these DNAs and found them to be overlapping. We selected the DNA sequence of Accession Number AC005961 to continue our efforts to obtain the sequence of our novel orexin- or NPY-like receptor (hereafter referred to as the “novel GPCR”).

8. BLAST analysis revealed that within AC005961 there were sequences comprising at least five exons with homology to the orexin-2 receptor. Exhibit 3 provides a copy of BLAST comparisons of five potential exons of an amino acid sequence of a putative novel GPCR encoded within Accession Number AC005961 (Sbjct) relative to the human orexin-2 receptor (Query) at page 1. Pages 2-3 of Exhibit 3 contain the description of the human orexin-2 receptor query sequence as found under Accession Number NP\_001517.

9. Prior to March 2, 2000, we used sequence information from AC005961 to begin cloning the novel GPCR. We designed primers to amplify a portion of the novel GPCR from human genomic DNA using the polymerase chain reaction (PCR). We obtained PCR products of 161 bp (“NSAN.seq” or “GA1”) and 234 bp (“GA2”) from amplification of the genomic DNA. The 161 bp amplicon included DNA from transmembrane domains (TM) 1 and 2 of the putative novel GPCR. The 234 bp product included sequence from TM 3 and 4 domains of the putative novel GPCR.

10. A copy of the nucleotide sequences of the two PCR products is attached as Exhibit 4. Page 1 of Exhibit 4 describes the 161 bp sequence, which is identified by the

Sequence ID “NSAN.seq”, as the “pcr of g3823006 GA1.” Page 2 of Exhibit 4 shows the sequence of “NSAN.seq.” Nucleotides 11-153 of the 161 base pair “NSAN.seq” amplification product are identical to nucleotides 167-309 of claimed SEQ ID NO: 1. Exhibit 5 provides an alignment of the “NSAN.seq” sequence with SEQ ID NO: 1. The first 10 and last 8 nucleotides of the 161 bp clone, which do not align with SEQ ID NO: 1, are not exonic sequence.

11. A description of the 234 bp amplification product, identified as “GA2” (see the Sequence ID), is provided on page 3 of Exhibit 4. Page 4 of Exhibit 4 provides the sequence of “GA2.” Nucleotides 29-191 of the sequence of the “GA2” are identical to nucleotides 340-502 of claimed SEQ ID NO: 1. See Exhibit 6 for an alignment of “GA2 with SEQ ID NO: 1. The first 28 and last 43 nucleotides of the 234 bp clone do not align and presumably represent intronic sequence.

12. We designed primers to the 5'- and 3'-regions of the 161 bp amplification product, and performed 5'- and 3'-RACE to begin our effort to obtain the full-length nucleotide sequence of the novel GPCR. The reverse primers used in the strategy to extend the 5'-sequence of the novel GPCR were termed “GA1-85B” and “GA1-126B.” These primers are shown on pages 2 and 3 of Leonid Zhelnin’s laboratory notebook no. RB53651; copies of Leonid Zhelnin’s laboratory notebook pages 2 and 3 are provided as Exhibit 7.

13. The sequence of the “GA1-85B” primer is shown on the right side at the top of page 2 of Leonid Zhelnin’s laboratory notebook. The sequence of the “GA1-126B” primer is shown on the right side at the top of page 2, beneath the sequence of the “GA1-85B” primer. Page 2 also shows the location of primers “GA1-85B” and “GA1-126B” on the 161 nucleotide sequence of “NSAN.seq”. The sequence of each primer on the 161 nucleotide sequence is

circled, and “GA1-85B” and “GA1-126B” is handwritten above the location of each primer on the sequence.

14. Page 3 of Leonid Zhelnin’s laboratory notebook shows the location of the primers “GA1-85B” and “GA1-126B” on an alignment of the 161 bp subregion of G3823006, “NSAN.seq” (“GA1”). The sequence of each primer on the 161 nucleotide sequence is circled, and “GA1-85B” and “GA1-126B” is handwritten below the location of each primer on the sequence. The locations of nested PCR primers are also indicated.

15. Exhibit 8 shows the location of the “GA1-85B” and “GA1-126B” RACE primers against SEQ ID NO:1. The shaded box indicates the position of the 161 bp fragment, NSAN.seq; the identities of amino acids of the codons represented within the primers are included for reference purposes.

16. Prior to March 2, 2000, using the “GA1-85B” and “GA1-126B” primers, we obtained two 5'-RACE clones (210 and 347 bp) from human heart cDNA that were used to extend the sequence further 5' to NSAN.seq (GA1). Assembly of sequence data from the 5'-RACE clones and the 161 bp clone, NSAN.seq, revealed a 347 bp long ORF, named 5GA1. The predicted 103 amino-acid peptide encoded by this ORF had significant homology to the N-terminal regions of the NPY-1 and orexin-2 receptors.

17. The sequence of the nucleotide and encoded polypeptide of the 347 bp ORF, 5GA1, are provided in Exhibit 9, which contains a copy of pages 47 and 48 of Leonid Zhelnin’s laboratory notebook no. RB53651. Page 47 (page 1 of Exhibit 9), shows the nucleotide and encoded polypeptide sequence of the 347 bp RACE clone (top), and a ClustalW-formatted alignment of the predicted amino acid sequence of 5GA1 with the amino acid sequence of the neuropeptide Y1 receptor (NPY-1R.pep) (bottom). Page 48 (page 2 of Exhibit 9) shows a

ClustalW-formatted alignment of the predicted amino acid sequence of 5GA1 with the amino acid sequence of the orexin-2 receptor (Orexin 2.pep).

18. An alignment of the amino acid sequence encoded by 5GA1 with SEQ ID NO: 2 is provided in Exhibit 10. The alignment indicates that the amino acid sequence encoded by 5GA1 is identical to amino acid residues 1-103 of SEQ ID NO: 2. The last two predicted residues of 5GA1 are not represented in SEQ ID NO: 2.

19. An alignment of the nucleotide sequence of 5GA1 to SEQ ID NO: 1 is provided in Exhibit 11. The alignment shows that the nucleotide sequence of the 5GA1 clone is identical to nucleotides 1 – 309 of SEQ ID NO: 1. The nucleotide sequence of 5GA1 further extended the 161 bp sequence of NSAN.seq, the initial PCR fragment identical to nucleotides 167-309 of SEQ ID NO: 1 (see paragraph 6 and alignment in Exhibit 5), to include nucleotides 1 – 166 of SEQ ID NO: 1.

20. The position of the putative START methionine codon (ATG) in clone 5GA1 was consistent with clone 5GA1 being similar to the NPY-1 and orexin-2 receptors. The identity of this ATG as the true START codon was, however, unconfirmed at this point in the cloning because the open reading frame (ORF) was not closed upstream of the 5'-most ATG.

21. Documentation of the initial efforts to perform 3'-RACE are provided as Exhibit 12, which contains copies of pages 4 and 5 of Leonid Zhelnin's laboratory notebook no. RB53651. These pages show the location of the "forward" primers termed "GA1-F32" and "GA1-F41." The nucleotide sequence of primer "GA1-F32" is shown at the bottom of page 4 of Leonid Zhelnin's laboratory notebook. The nucleotide sequence of primer "GA1-F41" is shown as the nucleotide sequence immediately above the nucleotide sequence of primer "GA1-F32."

22. Page 4 of Leonid Zhelnin's laboratory notebook, the first page of Exhibit 12, also shows the location of each of primers "GA1-F32" and "GA1-F41" in the sequence of the 161 nucleotide clone ("NSAN.seq" or "GA1"). The nucleotide sequence of each primer is circled on "NSAN.seq." "GA1F41" is also handwritten above its nucleotide sequence in "NSAN.seq." "6AF32" is handwritten to the side of the nucleotide sequence for "GA1-F32". Exhibit 8, described above in paragraph 15, also diagrams the location of the forward primers relative to SEQ ID NO: 1.

23. The amplification conditions for performing 3'-RACE are provided on page 5 of Leonid Zhelnin's laboratory notebook, which is page 2 of Exhibit 12. The product of 3'-RACE can be seen in a photograph of an agarose gel provided at the bottom right-hand corner of page 1 of Exhibit 12, see particularly lanes 3 and 4 from the left.

24. We analyzed the sequence of the 3'-RACE amplicon procedure, which revealed that this clone contained sequences homologous to a GPCR through the seventh transmembrane domain, and ended in a polyadenosine stretch but with no STOP codon. Exhibit 13 is an alignment of two independent 3'-RACE amplicons, LZLZ11 and LZLZ21, with the "5GA1" consensus sequence as recorded on page 53 of Leonid Zhelnin's laboratory notebook no. RB53651.

25. LZLZ11 and LZLZ21 are 650 bp and 730 bp in length, respectively. When these two amplicons of overlapping sequence (see Exhibit 13, described in paragraph 24 above) are linked through PCR amplification they yielded a clone (3'-RACE #2). The 3'-RACE #2 clone is 913 bp in length. An alignment of 3'-RACE #2 clone with SEQ ID NO: 1 is shown in Exhibit 14A: The 913 base pair sequence of the 3'-RACE #2 clone is identical to nucleotides 230-1017 of SEQ ID NO: 1. An alignment of the amino acid sequence encoded by 3'-RACE #2 with SEQ

ID NO: 2 is shown in Exhibit 14B. The amino acid sequence encoded by 3'-RACE #2 is identical to amino acid residues 78-339 of SEQ ID NO: 2.

26. Assembling, by computer, the sequence of 3'-RACE #2 clone and clone 5GA1, we predicated a hypothetical 1036-nucleotide sequence encoding 345 amino acids. The sequence of the “virtual” 1036-nucleotide clone is identical to nucleotides 1-1017 of SEQ ID NO: 1. An alignment of these sequences is shown in Exhibit 15. The nucleotide sequences of the individual LZLZ11, LZLZ21 and 5GA1 sequences, which comprise the 3'-RACE #2 clone, are separately highlighted in Exhibit 15, pages 1 and 2.

27. The apparent poly(A) tail of the 3'-RACE #2 clone is not found in SEQ ID NO: 1. The 345 amino acid sequence encoded by the virtual clone is identical to amino acid residues 1-339 of SEQ ID NO: 2. An alignment of the 345-amino acid sequence with SEQ ID NO: 2 is provided on page 3 of Exhibit 15. Given the fact that the 3'-RACE #2 clone (and, hence, the virtual clone) had no STOP codon and an abnormally short C-terminal intracellular domain, we predicted that we still needed to identify more 3' sequence to complete the clone. The potential STOP codon highlighted at the bottom right of page 53 of Leonid Zhelnin’s notebook no. RB53651 (Exhibit 13) actually is part of the Marathon-Ready™ cDNA adaptor in the vector.

28. Prior to March 2, 2000, we used the virtual sequence shown in Exhibit 13 as a template to search the Image Consortium database for novel expressed sequence tags (ESTs) to identify the missing 3'-nucleotide sequence. We identified three Image clones (named Im: 2055532, Im: 2055185, and Im: 2091776) from human kidney which had similarity to the virtual clone. Identification of the three Image clones was recorded at the top of page 61 of Leonid Zhelnin’s laboratory notebook no. RB53651 (Exhibit 16).

29. Sequence analysis of Image clone 2055185 confirmed the putative START methionine described in paragraph 20 because it revealed an in-frame STOP codon upstream of this START methionine. Page 89 of Leonid Zhelnin's laboratory notebook no. RB53651 shows the START and STOP codons of the assembled sequence (Exhibit 17). The in-frame "TAG" STOP codon is boxed and begins 111 bp upstream of the first nucleotide of the START methionine, which is marked with an "M" at nucleotide 394 of the sequence.

30. We again performed a BLAST search of the sequence contained in AC005961 (as described in paragraph 4 above) to obtain the 3'-most sequence of the novel GPCR. We used a short stretch of sequence as query (about twenty nucleotides). The query sequence was located between the site of a several hundred-nucleotide unspliced intron and a stretch of 8 adenosine residues found in the sequence near the 3'-end of one of the Image clones. The top portion of Exhibit 18 diagrams the BLAST search strategy. Done this way, it was hoped that the search algorithm would not miss critical homologies with this short region which might otherwise be lost because of relevant sequence being "diluted" within a larger query sequence potentially broken up by other unidentified unspliced introns.

31. BLAST analysis identified the 279 nucleotide region that contained the putatively complete 3'-end and STOP codon of the novel GPCR. This information is provided as nucleotides 1411-1689 of the sequence on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651 (Exhibit 19 is a copy of page 89 of Leonid Zhelnin's laboratory notebook, the full-length sequence is referred to as LGZ1.seq).

32. The 279 nucleotides are identical to nucleotides 1018-1296 of SEQ ID NO: 1. An alignment of the 3'-most 300 nucleotides (279 bp of coding and 21 bp of 3'-untranslated) of the full-length novel GPCR, LGZ1, with SEQ ID NO:1 is provided in Exhibit 20.

33. The coding region of the novel GPCR included 1,296 nucleotides separated into 6 exons within the 154,647 nucleotides of genomic sequence AC005961. Exhibit 18, bottom diagram, shows the genomic structure of the novel GPCR.

34. Prior to March 2, 2000, we amplified clones containing the complete 1296-bp ORF as well as 5'- and 3'-untranslated DNA from both human heart and brain cDNA by PCR (using Marathon-Ready cDNA libraries, Clontech). The complete sequence of the novel GPCR was recorded on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651. Exhibit 17, also described in paragraph 29, provides a copy of page 89 of Leonid Zhelnin's laboratory notebook. The 1296-bp ORF is identical to SEQ ID NO:1.

35. Also prior to March 2, 2000, we confirmed the coding sequence of the full-length cDNA clone by sequence analysis of a full-length amplicon generated by PCR from human brain cDNA. This sequence was recorded on pages 92 and 96-97 of Leonid Zhelnin's laboratory notebook no. RB53651; copies of these pages are provided as Exhibit 21.

36. The coding sequence obtained by the sequence analysis is contained within SEQ ID NO:1 of our provisional application Serial No. 60/216,523, which is identical to SEQ ID NO:1 of our utility application 09/899,532. Exhibit 22 shows the 100% identity between SEQ ID NO: 1 and nucleotides 19 – 1335 of the sequence shown in Exhibit 21.

37. The amino acid sequence encoded by nucleotides 19 – 1335 in Exhibit 21 is identical to SEQ ID NO: 2 of our provisional application Serial No. 60/216,523, which is identical to SEQ ID NO: 2 of our utility application 09/899,532. An alignment of SEQ ID NO: 2 of the provisional and utility applications with the amino acid sequence shown in Exhibit 21 is provided in Exhibit 23. In addition, an alignment of the amino acid sequence shown in Exhibit 21 showing the constructs used to assemble SEQ ID NO: 2 is shown in Exhibit 24.

38. All statements made herein of our own knowledge are true and all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated: January 31, 2005

Brian T. Bloomquist

Brian T. Bloomquist, Ph.D.

Dated: January 31, 2005

Leonid Zhelnin

Leonid Zhelnin

## Exhibit 1

# Identification of G3823006



## Analysis Results

Main Menu	Projects	Query	Seq Analysis	Utilities	Login / Logout	Help
-----------	----------	-------	--------------	-----------	----------------	------

Project ID: orexin Project Name: orexin receptor homology search  
 Created: Created By: Zhelnin, Leonid  
 Modified: Modified By: lt\_Account, Admin  
 Status: OPEN Current User: Zhelnin, Leonid (WRITE)  
 Today's Date: Num Seqs: 7

### Analysis Date:

These results are *saved*. Use the buttons to change the state of these results.

<input type="button" value="Save These Results"/>	<input type="button" value="Discard These Results"/>
---	--

Description:

### Maximum Number of Hits per Hit Class

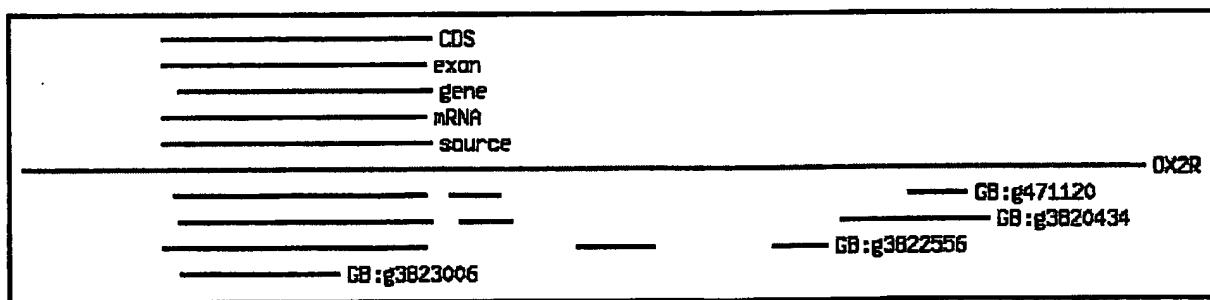
Trans. Protein:

Feature roll-up:  Off  On



### View parameters

#### Protein Agent



orexin:OX2R:1

Hit ID	P-Value	% ident.	Description		Hit Class
<input checked="" type="checkbox"/> GB:g471120:2	8.8e-19	34	Human mRNA for angiotensin II type 1b receptor, complete cds.		Trans. Protein
Result Details	Feature		Description	Feature Metric	Value

	CDS	Left End	Right End	Strand	Component Description	Component Metric	Value	
		61	160	+				
	source							
		Left End	Right End	Strand	Component Description	Component Metric	Value	
Result Details		61	160	+				
	Hit ID	P-Value	% ident.	Description				Hit Class
	<input checked="" type="checkbox"/> GB:g3820434:2	2.2e-18	30	Mus musculus mRNA for G-protein coupled receptor, complete CDS.				Trans. Protein
	Feature			Description			Feature Metric	Value
	CDS							
		Left End	Right End	Strand	Component Description	Component Metric	Value	
		62	162	+				
	gene							
		Left End	Right End	Strand	Component Description	Component Metric	Value	
		62	162	+				
Result Details	source							
		Left End	Right End	Strand	Component Description	Component Metric	Value	
		62	162	+				
	Hit ID	P-Value	% ident.	Description				Hit Class
	<input checked="" type="checkbox"/> GB:g3822556:1	3.6e-14	33	Bos taurus oxytocin receptor gene, promoter region and partial cds.				Trans. Protein
	Feature			Description			Feature Metric	Value
	CDS							
		Left End	Right End	Strand	Component Description	Component Metric	Value	
		56	160	+				
	exon							
Result Details		Left End	Right End	Strand	Component Description	Component Metric	Value	
		56	160	+				
	mRNA							
		Left End	Right End	Strand	Component Description	Component Metric	Value	
		56	160	+				
	source							
		Left End	Right End	Strand	Component Description	Component Metric	Value	
		56	160	+				
	Hit ID	P-Value	% ident.	Description				Hit Class
	<input checked="" type="checkbox"/> GB:g3823006:1	9.6e-10	39	HS_2052_B1_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=7 Row=N, genomic survey sequence.				Trans. Protein
	Feature			Description			Feature Metric	Value

source						
	Left End	Right End	Strand	Component Description	Component Metric	Value
	63	125	+			

Requested by: Zhelnin, Leonid





## Query Detail

Main Menu	Projects	Query	Seq Analysis	Utilities	Login / Logout	Help
-----------	----------	-------	--------------	-----------	----------------	------

Sequence: GB:g3823006:1



## Entries with the same Physical Sequence

Newpage:g3823006:1orexin:g3823006:1FASTA

## General Information About The Entry

Sequence ID	g3823006		
Version	1		
Sequence Description	HS_2052_B1_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=7 Row=N, genomic survey sequence.		
Database	GB GENBANK		
Database Description	Nucleotide and Protein Sequence Data Bank		
Molecule	DNA		
Database Division	GSS		
Entry Header Line	AQ270411	483 bp	DNA
Alternate Keys	LOCUS AQ270411 PRIMARY AC AQ270411		

## Sequence Information

Length	483
Sequence Header Line	155 a 84 c 169 g 73 t 2 others

## Origin and Alternate Names

Keywords	GSS
Organism	Homo sapiens
Taxonomy	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Species	HOMO SAPIENS
Biological Tissue Source	human.

## Comments

- Contact: Mahairas GG, Wallace JC, Hood L
- High Throughput Sequencing Center
- University of Washington
- 401 Queen Anne Avenue North, Seattle, WA 98109, USA
- Tel: (206) 616-3618
- Fax: (206) 616-3887
- Email: jwallace@u.washington.edu
- Sequence Tagged Connector
- Plate: 2052 row: N column: 7
- Class: BAC ends

- High quality sequence stop: 483.

**References**

[1]	(bases 1 to 483)
Title	Construction of a Characterized Clone Resource for Genomic Sequencing
Journal	Unpublished

Authors	Mahairas G.G. Wallace J.C. Smith K. Swartzell S. Furlong J. Shaker R. Schmidt S. Traicoff R. Hood L.E.
---------	--

**Hits and Features**Public Source**Public Source****Feature 1****source**

1..483  
1 .. 483 (+ strand)

**Feature Qualifiers**

clone Plate=2052 Col=7 Row=N  
clone\_lib CIT Approved Human Genomic Sperm Library D  
organism Homo sapiens

sex male

**Feature Cross References**

taxon 9606

**Feature Notes**

Organ: sperm; Vector: pBeloBAC11; BAC Clones in  
E-Coli DH10B



**INCYTE PHARMACEUTICALS, INC.**

## Exhibit 2

### Identification of AC005961



## Analysis Results

Main Menu	Projects	Query	Seq Analysis	Utilities	Login / Logout	Help
Project ID: <u>orexin</u>	Project Name: orexin receptor homology search					

Created: Created By: Zhelnin, Leonid

Modified: Modified By: lt\_Account, Admin

Status: OPEN Current User: Zhelnin, Leonid (WRITE)

Today's Date: Num Seqs: 7

### Analysis Date:

These results are *saved*. Use the buttons to change the state of these results.

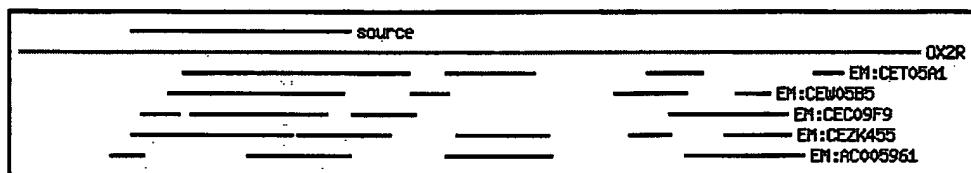
Description:

### Maximum Number of Hits per Hit Class

Trans. Protein:   
 Feature roll-up:  Off  On

[View parameters](#)

### Protein Agent



orexin:OX2R:1

Hit ID	P-Value	% ident.	Description				Hit Class
<input checked="" type="checkbox"/> EM:CE05A1:5	2.5e-17	40	Caenorhabditis elegans cosmid T05A1				Trans. Protein
Result Details	Feature	Description				Feature Metric	Value
	source					Component Metric	Value
		Left End	Right End	Strand	Component Description	Component Metric	Value
		81	134	+			
Hit ID	P-Value	% ident.	Description				Hit Class
<input checked="" type="checkbox"/> EM:CEW05B5:5	4.7e-17	33	Caenorhabditis elegans cosmid W05B5				Trans. Protein
Result Details	Feature	Description				Feature Metric	Value
	source					Component Metric	Value
		Left End	Right End	Strand	Component Description	Component Metric	Value

		74	133	+		
Hit ID	P-Value	% ident.	Description			Hit Class
<input checked="" type="checkbox"/> EM:CEC09F9:5	7.4e-17	35	Caenorhabditis elegans cosmid C09F9			Trans. Protein
Result Details		Feature	Description			Feature Metric
		source				Value
			Left End	Right End	Strand	Component Description
			85	152	+	Component Metric
						Value
Hit ID	P-Value	% ident.	Description			Hit Class
<input checked="" type="checkbox"/> EM:CEZK455:5	8.3e-14	26	Caenorhabditis elegans cosmid ZK455			Trans. Protein
Result Details		Feature	Description			Feature Metric
		source				Value
			Left End	Right End	Strand	Component Description
			56	134	+	Component Metric
						Value
Hit ID	P-Value	% ident.	Description			Hit Class
<input checked="" type="checkbox"/> EM:AC005961:1	1.8e-12	32	*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase 1, 8 unordered pieces.			Trans. Protein
Result Details		Feature	Description			Feature Metric
		source				Value
			Left End	Right End	Strand	Component Description
			112	163	+	Component Metric
						Value

Select All  Deselect All

Save to Project  Submit  Reset

Requested by: Zhelnin, Leonid

 INCYTE PHARMACEUTICALS, INC.



## Project Summary

Main Menu	Projects	Query	Seq Analysis	Utilities	Login / Logout	Help
-----------	----------	-------	--------------	-----------	----------------	------

Project ID: orexin Project Name: orexin receptor homology search  
 Created: Created By: Zhelnin, Leonid  
 Modified: Modified By: lt\_Account, Admin  
 Status: OPEN Current User: Zhelnin, Leonid (WRITE)  
 Today's Date: Num Seqs: 7

<a href="#">Project Members</a>	<a href="#">Project Status</a>
<a href="#">Analysis Tools</a>	<a href="#">Create Agent</a>

### Sequences (7 of 7 shown, 7 Active):

Sequence ID	Type	Parent	Created By	Created	Status
<u>orexin:g3823006:1</u>	DNA	<u>GB:g3823006</u>	Zhelnin, L.		OPEN
HS_2052_B1_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=7 Row=N, genomic survey sequence.					
<u>orexin:AC005961:1</u>	DNA	<u>EM:AC005961</u>	Zhelnin, L.		OPEN
*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase 1, 8 unordered pieces.					
<u>orexin:frame1_AC005961:1</u>	PRT		Zhelnin, L.		OPEN
<u>orexin:neworex1.pep:1</u>	PRT		Zhelnin, L.		OPEN
<u>orexin:G2897124:1</u>	PRT	<u>ST:G2897124</u>	Zhelnin, L.		OPEN
OREXIN RECEPTOR-1.					
<u>orexin:OX2R:1</u>	PRT		Zhelnin, L.		OPEN
P1;G2897128 - orexin receptor-2 - Homo sapiens (human)					
<u>orexin:AF041243:1</u>	RNA	<u>EM:AF041243</u>	Zhelnin, L.		OPEN
Homo sapiens orexin receptor-1 mRNA, complete cds.					

<a href="#">Manage Sequences</a>	<a href="#">Add Sequence</a>
----------------------------------	------------------------------

### Gene Agent Results (10 of 166 shown, 166 active):

Agent Name	Results	Started On	Description	Status	Method	Job Status
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed

<a href="#">List All Gene Agent Results</a>
---

*Query Detail*

Main Menu   Projects   Query   Seq Analysis   Utilities   Login / Logout   Help

Sequence: orexin:AC005961:1   [Add Sequence Annotation](#)



## Entries with the same Physical Sequence

[Imagelga:g3859648:1](#)[Newgag:AC005961:1](#)[FASTA](#)

## General Information About The Entry

Sequence ID	AC005961
Version	1
Sequence Description	*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase 1, 8 unordered pieces.
Project	orexin
Project Name	orexin receptor homology search
Molecule	DNA
Sequence Information	
Length	154647

 INCYTE PHARMACEUTICALS, INC.

## Exhibit 3

Homology between  
AC005961 and the orexin-2  
receptor

Sequences producing High-scoring Segment Pairs:		Reading Frame	High Score	Proba P(N)
AC005961 *** SEQUENCING IN PROGRESS *** Homo sapien..		+2	103	1.8e-
Score = 103 (48.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12				
Identities = 17/52 (32%), Positives = 33/52 (63%), Frame = (+2)				
Query: 112	LVVDITETWFFGQSLCKVIPYLQTVSVSVSVLTLSCIALDRWYAICHPLMFK	163		
	L+ D++ G +CK++P++Q+ +V +LT++CIA++R + HP K			
Sbjct: 48452	LMYDLSYFLTAGAFICKMVPFVQSTAVVTEILTMTCIAVERHQGLVHPFKMK	48607		
Score = 88 (41.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12				
Identities = 15/54 (27%), Positives = 31/54 (57%), Frame = (+3)				
Query: 210	CDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKWLWCRQIPGTSSVVQ	263		
	C E W ++ K+Y ++ ++ PL +M++ Y +I +LW ++ G SV++			
Sbjct: 56082	CLEEWTSVPHQKIQYTTFILVILFLLPLMVMLILYSKIGYELWIKKRVDGSVLR	56243		
Score = 71 (33.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12				
Identities = 15/54 (27%), Positives = 26/54 (48%), Frame = (+1)				
Query: 329	VFGMFAHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSGKFREEFKAAFSCC	382		
	+ G F D T+ F + ++NS NPI+Y F++ F++ +A C			
Sbjct: 59380	ISGNFEKEYDDVTIKMIFAIVQIIGFSNSICNPIVYAFMNENFKKNVLSAVCYC	59541		
Score = 47 (22.1 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12				
Identities = 9/17 (52%), Positives = 11/17 (64%), Frame = (+2)				
Query: 46	EYLHPKEYEWVLIAGYI	62		
	EY H +E W LI+ YI			
Sbjct: 29786	EYPHAE*NWTLISQYI	29836		
Score = 46 (21.6 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12				
Identities = 6/8 (75%), Positives = 7/8 (87%), Frame = (+3)				
Query: 381	CCCLGVHH	388		
	CCCLG+ H			
Sbjct: 148296	CCCLGLEH	148319		

NCBI   Protein

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD

1: [NP\\_001517](#). Reports orexin receptor 2...[gi:4557639] [BLINK](#), [Domains](#), [Links](#)

LOCUS NP\_001517 444 aa linear PRI

DEFINITION orexin receptor 2 [Homo sapiens].

ACCESSION NP\_001517

VERSION NP\_001517.1 GI:4557639

DBSOURCE REFSEQ: accession NM\_001526.2

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 444)

AUTHORS Karteris,E., Chen,J. and Randeva,H.S.

TITLE Expression of human prepro-orexin and signaling characteristics of orexin receptors in the male reproductive system

JOURNAL J. Clin. Endocrinol. Metab. 89 (4), 1957-1962 (2004)

PUBMED 15070969

REMARK GeneRIF: both OX1R and OX2R are expressed in the testis, epididymis, penis, and seminal vesicle

REFERENCE 2 (residues 1 to 444)

AUTHORS Peyron,C., Faraco,J., Rogers,W., Ripley,B., Overeem,S., Charnay,Y., Nevsimalova,S., Aldrich,M., Reynolds,D., Albin,R., Li,R., Hungs,M., Pedrazzoli,M., Padigaru,M., Kucherlapati,M., Fan,J., Maki,R., Lammers,G.J., Bouras,C., Kucherlapati,R., Nishino,S. and Mignot,E.

TITLE A mutation in a case of early onset narcolepsy and a generalized absence of hypocretin peptides in human narcoleptic brains

JOURNAL Nat. Med. 6 (9), 991-997 (2000)

PUBMED 10973318

REFERENCE 3 (residues 1 to 444)

AUTHORS Sakurai,T., Amemiya,A., Ishii,M., Matsuzaki,I., Chemelli,R.M., Tanaka,H., Williams,S.C., Richardson,J.A., Kozlowski,G.P., Wilson,S., Arch,J.R., Buckingham,R.E., Haynes,A.C., Carr,S.A., Annan,R.S., McNulty,D.E., Liu,W.S., Terrell,J.A., Elshourbagy,N.A., Bergsma,D.J. and Yanagisawa,M.

TITLE Orexins and orexin receptors: a family of hypothalamic neuropeptides and G protein-coupled receptors that regulate feeding behavior

JOURNAL Cell 92 (5), 1 (1998)

PUBMED 9527442

REFERENCE 4 (residues 1 to 444)

AUTHORS Sakurai,T., Amemiya,A., Ishii,M., Matsuzaki,I., Chemelli,R.M., Tanaka,H., Williams,S.C., Richardson,J.A., Kozlowski,G.P., Wilson,S., Arch,J.R., Buckingham,R.E., Haynes,A.C., Carr,S.A., Annan,R.S., McNulty,D.E., Liu,W.S., Terrell,J.A., Elshourbagy,N.A., Bergsma,D.J. and Yanagisawa,M.

TITLE Orexins and orexin receptors: a family of hypothalamic neuropeptides and G protein-coupled receptors that regulate feeding behavior

JOURNAL Cell 92 (4), 573-585 (1998)

PUBMED 9491897

REFERENCE 5 (residues 1 to 444)

AUTHORS Flier,J.S. and Maratos-Flier,E.

TITLE Obesity and the hypothalamus: novel peptides for new pathways

JOURNAL Cell 92 (4), 437-440 (1998)

PUBMED 9491885

REFERENCE 6 (residues 1 to 444)

AUTHORS de Lecea,L., Kilduff,T.S., Peyron,C., Gao,X., Foye,P.E., Danielson,P.E., Fukuhara,C., Battenberg,E.L., Gautvik,V.T.,

Bartlett, F.S. II, Frankel, W.N., van den Pol, A.N., Bloom, F.E.,  
 Gautvik, K.M. and Sutcliffe, J.G.

**TITLE** The hypocretins: hypothalamus-specific peptides with neuroexcitatory activity

**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 95 (1), 322-327 (1998)

**PUBMED** 9419374

**COMMENT** REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AF041245.1.

**Summary:** HCRTR2 is a G-protein coupled receptor expressed exclusively in the brain. It has 64% identity with HCRTR1. HCRTR2 binds both orexin A and orexin B neuropeptides. HCRTR2 is involved in the central feedback mechanism that regulates feeding behaviour.

**FEATURES** Location/Qualifiers

**source** 1..444  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="6"  
 /map="6p11-q11"

**Protein** 1..444  
 /product="orexin receptor 2"  
 /note="orexin receptor-2; hypocretin receptor-2"

**CDS** 1..444  
 /gene="HCRTR2"  
 /coded\_by="NM\_001526.2:325..1659"  
 /note="go\_component: integral to plasma membrane [goid 0005887] [evidence TAS] [pmid 9491897];  
 go\_function: orexin receptor activity [goid 0016499] [evidence IEA];  
 go\_function: rhodopsin-like receptor activity [goid 0001584] [evidence IEA];  
 go\_function: neuropeptide receptor activity [goid 0008188] [evidence TAS] [pmid 9491897];  
 go\_process: feeding behavior [goid 0007631] [evidence TAS] [pmid 9491897];  
 go\_process: synaptic transmission [goid 0007268] [evidence TAS] [pmid 9491897];  
 go\_process: neuropeptide signaling pathway [goid 0007218] [evidence TAS] [pmid 9491897]"  
 /db\_xref="GeneID:3062"  
 /db\_xref="LocusID:3062"  
 /db\_xref="MIM:602393"

**ORIGIN**

```

1 msGTKledsp pcrnwssase lnetqepfln ptdydddeefl rylwreylhp keyewvliag
61 yiivfvvali gnvlvcvaww knhhmrvtvn yfivnislad vlvtitclpa tlvvvitew
121 ffgqslckvi pylqtvsвш svltlscial drwyachpl mfkstakrar nsiviiwivs
181 ciimipqaiv mectvfpfpgl ankttifftvc derwgeiyp kmyhicfflv tymaplclmv
241 laylqifrk1 wcrqipgtss vvqrkwpklq pvsqprgpgq ptksrmsava aeikqirarr
301 ktarmlmvvl lvfaicylpi silnvlkrfv gmfahetedre tvyawftfsh wlvyansaan
361 piynflsgk freefkaafs ccclgvhhrq edrltrgrts tesrkslttq isnfdniskl
421 seqvvltsis tipaangagp lqnw
  //
```

[Disclaimer](#) | [Write to the Help Desk](#)  
 NCBI | NLM | NIH

## Exhibit 4

Description of the 161 bp  
fragment (NSAN.seq or  
GA1) and 234 bp fragment  
(GA2)

*Query Detail*

---

Main Menu   Projects   Query   Seq Analysis   Utilities   Login / Logout   Help

---

Sequence: **Newgage:NSAN.seq:1**   [Add Sequence Annotation](#)[Sequence View](#)

Entries with the same Physical Sequence		FASTA
<b>General Information About The Entry</b>		
Sequence ID	NSAN.seq	
Version	1	
Sequence Description	pcr of g3823006 GA1	
Project	Newgage	
Project Name	Cloning new gene agent search sequences	
Molecule	DNA	
<b>Sequence Information</b>		
Length	161	

---

 **INCYTE PHARMACEUTICALS, INC.**



## Retrieve FASTA Sequences

Main Menu   Projects   Query   Seq Analysis   Utilities   Login / Logout   Help

Project ID: Newgage      Project Name: Cloning new gene agent search sequences  
Created:      Created By: Zhelnin, Leonid  
Modified:      Modified By: Zhelnin, Leonid  
Status:      OPEN      Current User: Zhelnin, Leonid (WRITE)  
Today's Date:      Num Seqs:      30

>Newgage:NSAN.seq:1    pcr of g3823006 GA1  
AGTGTACTCATGCCCTGGCGCTTTGGCAATGCTCTGGTGTCTACGTGGTGACCCGAGCAAGGCCATGCGCACCGT  
CACCAACATTTATCTGCTCCTGGCGCTCAGTGACCTGCTCATCACCTTCTGCATTCCGTACCATGAAGCCGA  
A

Requested by: Zhelnin, Leonid

 INCYTE PHARMACEUTICALS, INC.

**Query Detail**

Main Menu	Projects	Query	Seq Analysis	Utilities	Login / Logout	Help
-----------	----------	-------	--------------	-----------	----------------	------

Sequence: **Newgage:GA2:1** [Add Sequence Annotation](#)

Entries with the same Physical Sequence		FASTA
<b>General Information About The Entry</b>		
Sequence ID	GA2	
Version	1	
Sequence Description	pcr product of ac acl primers of AC00596 genomic chromosome seq in progress	
Project	Newgage	
Project Name	Cloning new gene agent search sequences	
Molecule	DNA	
<b>Sequence Information</b>		
Length	234	

 **INCYTE PHARMACEUTICALS, INC.**



## Retrieve FASTA Sequences

Main Menu   Projects   Query   Seq Analysis   Utilities   Login / Logout   Help

Project ID: Newgage  
Created:  
Modified:  
Status:      OPEN  
Today's Date:

Project Name: Cloning new gene agent search sequences  
Created By: Zhelnin, Leonid  
Modified By: Zhelnin, Leonid  
Current User: Zhelnin, Leonid (WRITE)  
Num Seqs: 30

>Newgage:GA2:1      pcr product of ac ac1 primers of AC00596 genomic chromosome se  
GTATGATTATCCTATTCCTTACTGCAGGTGCTTCATTGCAAGATGGTGCCATTGCTCCAGTCTACCGCTGTTGTGA  
CAGAAATCCTCACTATGACCTGCATTGCTGTGGAAAGGCACCAGGGACTTGTGCATCCTTTAAAATGAAGTGGCAATAC  
ACCAACCGAAGGGCTTCACAATGCTAGGTGAGGCCACTGGATGTGCCAATGGCAGTGTGAATGACATTCTCA

Requested by: Zhelnin, Leonid



## Exhibit 5

Nucleotide sequence  
comparison of NSAN.seq to  
SEQ ID NO 1

1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTC CGG GAC CAC AAC CTG ACG CGG GAG CAG TTC 75  
1 M Q A L N I T P E Q F S R L D H N L T R E Q F 25

76 ATC GCT CTG TAC CGG CTG CGA CGG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC 150  
26 I A L Y R L R P L V Y T P E L P G R A K L A L V L 50

AGTGTACTCA

151 ACC GGC GTG CTC ATC TTC CGC CGC CTC TTT GGC AAT GCT CTG GTG ACC CGC AGC AAG GCC 225  
51 T G V L I F A L F G N A L V F Y V V T R S K A 75

*TM1*

ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TGG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC  
226 ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TGG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC  
76 M R T V T N I F I C S L A L S D L I T F F C I P 300  
101 V T M L Q N I S D N W L G G A F I C K M V P F V Q 125

*TM2*

AAGCCGAA

GTC ACC ATG  
301 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG 375  
101 V T M L Q N I S D N W L G G A F I C K M V P F V Q 125

376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 450  
126 S T A V V T E I L T M T C I A V E R H Q G L V H P 150

*TM3*

451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC ATC 525  
151 F K M K W Q Y T N R R A F T M L G V V W L V A V I 175

*TM4*

526 GAA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA ATT GAC ACC TTC CTA TAT GAA AAG GAA CAC ATC TGG 600  
176 V G S P M W H V Q Q L E I K Y D F L Y E K E H I C 200

601 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTC ATC CTC CTC CTG 675  
201 C L E W T S P V H Q I L Y S K I G Y E L W I K K R V G D G 225

*TM5*

676 CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 750  
226 P L M V M L I L Y S K I G Y E L W I K K R V G D G 250

751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAA CGA GCT GTC ATT ATG ATG 825  
251 S V L R T I H G K E M S K I A R K K R V I M M 275

826 GTG ACA GTG GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT AAT 900  
276 V T V A L F A V C W A P F H V V H M M I E Y S N 300

---

*TM6*

901 TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC 975  
301 F E K E Y D D V T I K M I F A I V Q I I G F S N S 325

---

*TM7*

976 ATC TGT AAT CCC ATT GTC TAT GCA TTT ATG AAT GAA AAC TTC AAA AAA AAT GTT TTG TCT GCA GTT TGT TAT TGC 1050  
326 I C N P I V Y A F M N E N F K N V L S A V C Y C 350

1051 ATA GTA AAT AAA ACC TTC TCT CCA GCA OAA AGG CAT GGA ATT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 1125  
351 I V N K T F S P A Q R H G N S G I T M M R K K A K 375

1126 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC ACT GAT GGC AAC ATT GAA GTC AAA TTG 1200  
376 F S L R E N P V E T K G E A F S D G N I E V K L 400

1201 TGT GAA CAG ACA GAG GAG AAA AAG CTC AAA CGA CAT CTC GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 1275  
401 C E Q T E E K K L K R H L A L F R S E L A E N S 425

1276 CCT TTA GAC AGT GGG CAT TAA 1296  
426 P L D S G H \* 431

## Exhibit 6

Alignment of 234 bp  
fragment to SEQ ID NO 1

1 ATG CAG GCG CTT AAC ATT ACC CCC GAG CAG TTC TCT CCG CTC CGG GAC CAC AAC CTC ACG CGG GAG CAG TTC 75  
 1 M Q A L N I T P E Q F S R L L R D H N L T R E Q F 25

76 ATC GCT CTG TAC CGG CTG CGA CCG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG CTC GTG CTC 150  
 26 I A L Y R L R P L V Y T P E L P G R A K L A L V L 50

151 ACC GGC GTG CTC ATC TTC GCC CTG GCG CTC TTT GGC AAT GCT CTG GTG TAC GTG GTG ACC CGC AGC AAG GCC 225  
 51 T G V L I F A L A L F G N A L V F Y V V T R S K A 75

---

*TM1*

226 ATG CGC ACC GTC ACC AAC ATC ATC TTT ATC TGC TCC TGG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC 300  
 76 M R T V T N I F C S L A L S D L I T F C I P 100

---

*TM2*

GTATGATTATCCATTCTTACTGCA  
 301 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTC ATT GCT TTC ATT TGC AAG ATG GTG CCA ATT GTC CAG 375  
 101 V T M L Q N I S D N W L G G A F I C K M V P F V Q 125

TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GCA ATT GTC CTT GTG CAT CCT 450  
 376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GCA ATT GTC CTT GTG CAT CCT  
 126 S T A V V T E I L T M T C I A V E R H Q G L V H P 150

---

*TM3*

AGGGCCACTGATGTGCCAATGCCAGGTGTGAATGACATTCTTCA  
 526 GTA GGA TCA CCC ATG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA ATT GCT G 525  
 451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA ATT GCT GTC TGG CTG GTG GCA GTC ATC  
 151 F K M K W Q Y T N R R A F T M L G V V W L V A V I 175

---

*TM4*

526 GTA GGA TCA CCC ATG TGG CAC GTC GAA CAA CTT GAG ATC AAA ATT GCT GAA ATT GGT TAT GAA AAG GAA CAC ATC TGC 600  
 176 V G S P M W H V Q Q L E I K Y D F L Y E K E H I C 200

---

*TM5*

601 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTC ATC CTC TTC CTC CTG 675  
 201 C L E E W T S P V H Q K I Y T T F I L V I L F L L 225

---

*TM5*

676 CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA ATT GGT GAA CTT TGG ATA AAG AAA AGA ATT GGG GAT GGT 750  
 226 P L M V N L I L Y S K I G Y E L W I K K R V G D G 250

---

*TM5*

751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAA CGA GCT GTC ATT ATG ATG 825  
 251 S V L R T I H G K E M S K I A R K K R A V I M M 275

826 GTG ACA GTG GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT AAT 900  
276 V T V V A L F A V C W A P F H V V H M M I E Y S N 300

*TM6*

901 TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC 975  
301 F E K E Y D D V T I K M I F A I V Q I I G F S N S 325

*TM7*

976 ATC TGT ATT CCC ATT GTC TAT GCA TTT ATG ATT GAA AAC TTC AAA AAA ATT GTT TTG TCT GCA GTT TGT TAT TGC 1050  
326 I C N P I V Y A F M N E N F K K N V L S A V C Y C 350

1051 ATA GTA ATT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 1125  
351 I V N K T F S P A Q R H G N S G I T M M R K K A K 375

1126 TTT TCC CTC AGA GAG ATT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG 1200  
376 F S L R E N P V E T K G E A F S D G N I E V K L 400

1201 TGT GAA CAG ACA GAG GAG AAG CTC AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 1275  
401 C E Q T E E K K K L K R H L A L F R S E L A E N S 425

1276 CCT TTA GAC AGT GGG CAT TAA  
426 P L D S G H \* 1296  
431

## Exhibit 7

### RACE primers

## BAYER CORPORATION

SUBJECT

5' RACE 64

1	9	1	85	85	54.1	74.1	4.9	54.1	56.8	61.7	48.1	60.0	-8.3	7.9	
2	+	CCATCTTAATAGACTCACTATAAGGC	27	-43.0	-205.0	-536.4		GGTCACCAAGTAGACACAGAGC	25	-41.9	-184.5	-470.9			6A1-85E
3	+	10	1	126	126	54.8	77.0	1.7	56.0	56.8	58.6	48.1	48.0	-8.3	-7.8
4	+	CCATCTTAATAGACTCACTATAAGGC	27	-43.0	-205.0	-536.4		GCAGATAAAGATGTGGTGACGGT	25	-40.2	-182.9	-471.0			6A1-126S
5															
6															
7															
8															
9															6C1CTT
10															
11															
12															
13															
14															
15															
16															
17															
18															
19															
20															
21															
22															
23															
24															
25															
26															
27															
28															
29															
30															
31															
32															
33															
34															

GA1.txt Translated Sequence

Sequence Range: 1 to 161

double strand probe

6A1-85B

6A1-FY1

6A1-85B  
 10 20 30 40 50  
 CACCTCTGTC ACCGG AGTGTACTCATGCCCTGGCCCTCTTGCAATGCCTCTGGTGTCTAGT  
 TCACATGAGTAGCGGGACCGCGAGAAACCGTTACGAGACCAAGATGCA  
 S V L I A L A L F G N A L V F Y V >

TRANSLATION OF GA1.TXT [A] &gt;

6A1-126B  
 60 70 80 90 100  
 GGTGACCCGAGCAAGCCATGCCACCGTCACCAACATCTTATCTGCT  
 CCACTGGCGCTCGTCCGGTACCGTGGCAGTGGTTGTAGAAATAGACGA  
 V T R S K A M R T V T N I F I C >

TRANSLATION OF GA1.TXT [A] &gt;

6A1-1B 6A1-BA2 6A1-BA1 (engp2)  
 110 120 130 140 150  
 CCTTGGCGCTCAGTGACCTGCTCATCACCTTCTCTGCATTCCCGTCACC  
 GGAACCGGGAGTCACGGACGAGTAGTGGAAAGAAGACGTAAGGGCAGTGG  
 S L A E S D E F F C I P V T >

TRANSLATION OF GA1.TXT [A] &gt;

160  
 ATGAAGCCGAA  
 TACCTCGGCTT  
 M K P X >

5 primers for 5' RACE

probe:

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

CROSS REFERENCES:

# **BAYER CORPORATION**

**SUBJECT**

GB g3823006. by GA1.txt Aligned Sequence

Sequence Range: 1 to 481

GB g382300 10 20 30 40 50 60 70 80 90 100  
ACGCGCGAAAGATGACCTCGTGTACCGGAGTGTACTCATGCCCTGGCG  
TCGCGCGTCTACTGGAGCACAGTGGCTCACATGAGTACGGAGCGCG

impl str +

GB g382300

jmp1 str + TCTTGCGC TCTTAGCAAATGCTTGGTGTTACAGTGGTACCGAGCAGCAAGACCATG  
GB g382300 TCTTAGCAAATGCTTGGTGTTACAGTGGTACCGAGCAGCAAGACCATG

jmp1 str + 6A1-126B } 6A1-Nest. 120 CAGTGACCTGCTC>  
GB g382300 6A1-1B ||| TCAGTGACTGCTC

GB g382300 ATCACCTTCTCTGCATTCCCGTCACCATGCTCCAGAA

CATC

'NOLDS / NILES, MI 'SEPT. 95

**SIGNED BY**

**DATE**

**WITNESSED AND UNDERSTOOD BY**

Tea in China

**DATE** \_\_\_\_\_

## Exhibit 8

Locations of RACE primers  
on SEQ ID NO 1

1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TMC TCT CGG CTG CGG GAC CAC AAC CTG ACG CGG GAG CAG TTC 75

76 ATC GCT CTG TAC CGG CTG CGA CCG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC 150

151 ACC GGC GTC CTC ATC **TTC** GGC CTC **TTC** GGC AAT GCT CTG GTG TAC **GTC** ACC CGC AGC AAG GCC 225

(L F G N A L V F Y)  
 CTC **TTC** GGC AAT GCT CTG GTG TAC **GTC** ACC CGC AGC AAG GCC  
 CGA GAC CAC AAG ATG CAC CAC TGG G  
 (A L V F Y V V T R)

GA1-F41

GA1-85B

226 **ATG** CGC ACC GTC ACC AAC ATC **TTC** ATC TGC **TTC** GTC TCC **TTC** GCG CTC AGT GAC CTG CTC ATC ACC TTC **TTC** TGC ATT CCC 300

(R T V T N I F I C)  
 G TGG CAG TGG TAG AAA TAG ACG  
 (R T V T N I F I C)

GA1-F32

GA1-126B

301 **[GTC ACC ATG]** CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG 375

376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 450

451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC ATC 525

526 GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGG 600

601 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTC ATC CTC TTC CTC CTG 675

676 CCT CTT ATG GTG ATG CTT ATT CTG TAC ATG AAA ATT GGT ATT GAA ATT TGG ATA AAG AAA AGA ATT GGG ATT GGT 750

751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAA CGA GCT GTC ATT ATG ATG 825

826 GTG ACA GTG GTG GCT CTC **TTC** GTG TGC TGG GCA CCA TTC CAT ATT GAA TAC AGT ATT GGT ATT GCA ATT ATG ATG 900

901 TTT GAA AAG GAA ATT GAT GAT GTC ACA ATC AAG ATG ATT TTC GCT ATC GTG CAA ATT ATT GGA ATT ATT GCA ATT ATT TCC AAC TCC 975

976 ATC TGT AAT CCC ATT GTC TAT GCA TTT ATG AAT GAA AAC TTC AAA AAA AAT GTT TTG TCT GCA GTT TGT TAT TGC 1050  
1051 ATA GTA AAT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA AAT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 1125  
1126 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GCA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG 1200  
1201 TGT GAA CAG ACA GAG GAG AAG AAA AAG CTC AAA CGA CAT CTC GCT GCT GTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 1275  
1276 CCT TTA GAC AGT GGG CAT TAA 1296

## Exhibit 9

5GA1 vs. NPY1 and OX-2

# **BAYER CORPORATION**

**SUBJECT**

## 6A1-5' RACE product

© 2000 DNA Spider™ 1.2

### Untitled Sequence # 1 > Genes

## 5GA1 Aligned Sequences Formatted Alignments

## ClustalW Formatted Alignments

5GA1 NPY-1R.pep M Q A L N I T P E Q F S R E L R D H N L T R E F F L Y R  
 M N S T L F S Q V E N H S W H S N F S E K N A L F F E N

5GA1            L R P L V Y T P E D P G R A K L A V P G V L I F A G A L  
*NPY-1R.pep* D - - - - D C H D P L A M I F D A A Y G A V I I N G V

5GA1 NPY-1R.pep F A L Y F Y V V T R S K A R M N H N F C S T A L S F 70 80 90

5GA1 NPY-1R.pep 100 V M K P 110 120

**SIGNED BY**

DATE

**WITNESSED AND UNDERSTOOD BY**

DATE

# BAYER CORPORATION

SUBJECT 6/21/02 RACE

Orexin 2.pep Aligned Sequences Formatted Alignments

## ClustalW Formatted Alignments

Orexin 2.pep 10 20 30  
5GA1 M S G T K E D S P C N W S S A S E L N E H Q V P E N  
M Q A L N T - - - P E Q F S R L L R H Q L R Q D A

Orexin 2.pep 40 50 60  
5GA1 P T D Y D D E E F Y W R E Y L H K E Y E W V R A G  
L Y R - - - - L R P V Y T P E L G R A K L A Y L T

Orexin 2.pep 70 80 90  
5GA1 Y T P Y V V A I V C V A N W N H H R T Y T N  
G V I I A A F A A F Y V M T R S K A M R A Y E

Orexin 2.pep 100 110 120  
5GA1 Y V N S A D V I N I T F A V V D I T E T W  
I P C S A S D I I F F V M K P

22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34

gil4758820 neuropeptide G protein-coupled receptor gb|AAD22047.11  
(AF119815) G-protein-coupled receptor [Homo sapiens]  
Length = 522

Score = 152 (73.0 bits), Expect = 1.8e-13, P = 1.8e-13  
Identities = 27/55 (49%), Positives = 42/55 (76%)

Query: 49 VLTGVLLIFALALPGNALVFPVVTRSKAMRTVTNIFICSLALSDDLITFFCIPVTM 103  
+++ LIF L + GN +V ++V R+K M TVTN+FI +LA+SDLL+ FC+P+T+  
Sbjct: 151 IISYFLIFLCLMGNITVVCFTIVMRNKHMTVTNLFILNLASDLVGIFCPMTL 205

>>SP:NY2R\_PIG NEUROPEPTIDE Y RECEPTOR TYPE 2 (NPY2-R). (383 aa)  
initn: 123 initl: 123 opt: 181 Z-score: 234.1 expect(): 2.5e-06  
Smith-Waterman score: 181; 45.100% identity in 71 aa overlap

10 20 30 40 50 60  
gal PEQFSRLLRDNLTREQFIALYRLRPLVYTPPELPGRAKLA-----LVLTGVLLIFALALFG  
SP:NY2R\_PIG DENQTVEEKMHEPSPGPGHTTPRGEELAPDSEPELKDSTKL18VQIILILAYCSILLGVVG

10 20 30 40 50 60  
gal 70 80 90 100  
NALVFPVVTRSKAMRTVTNIFICSLALSDDLITFFCIPVTKP  
SP:NY2R\_PIG 70 80 90 100 110 120  
NSLVIHVVIKFKMSRTVTFNFFIANLAVADLLVNTLCLPFTLTYTLMGEWKGMPVLCVLP

SP:NY2R\_PIG 130 140 150 160 170 180  
YAQGLAVQVSTITLTIVIALDRHRCIVYHLESKISKRISFLIIGLAWGISAASPLAIFR

SIGNED BY \_\_\_\_\_

DATE \_\_\_\_\_

WITNESSED AND UNDERSTOOD BY Leanne Zitman

DATE \_\_\_\_\_

CROSS REFERENCES: \_\_\_\_\_

## Exhibit 10

Alignment of 5GA1 with  
SEQ ID NO 2



## Exhibit 11

Alignment of 5GA1  
nucleotide sequence with  
SEQ ID NO 1

1 GGTGGCCCGGGGGAGGGAGAGCA 30  
 31 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTC GAC CAC AAC CTG ACG CGG GAG CAG TTC 105  
 1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTC GAC CAC AAC CTG ACG CGG GAG CAG TTC 75  
 1 M Q A L N I T P E Q F S R L L R D H N L T R E Q F 25  
 106 ATC GCT CTG TAC CGG CTG CGA CCG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC 180  
 76 ATC GCT CTG TAC CGG CTG CGA CCG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC 150  
 26 I A L Y R L R P L V Y T P E L P G R A K L A L V L 50  
 181 AC GC GC GTG CTC ATC TTC GCC CTC GCG CTC TTT GCC AAT GCT CTG GTG TTC TAC GTG GTG ACC CGC AGC AAG GCC 255  
 151 AC GC GC GTG CTC ATC TTC GCC CTC GCG CTC TTT GCC AAT GCT CTG GTG TTC TAC GTG GTG ACC CGC AGC AAG GCC 225  
 51 T G V L I F A L F G N A L V F Y V V T R S K A 75  
 256 ATG CGC ACC GTC ACC AAC ATC ATC TTC ATC TGC TCC TGC AGT GAC CTG CTG ATC ACC TTC TAC TGC ATT CCC 330  
 226 ATG CGC ACC GTC ACC AAC ATC ATC TTC ATC TGC TCC TGC AGT GAC CTG CTG ATC ACC TTC TAC TGC ATT CCC 300  
 76 M R T V T N I F I C S L A L S D L L I T F F C I P 100  
 347  
 301 GTC ACC ATG ATG GCG GAA CTC CAG AAC ATT TCC GAC AAC TGG CTC GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTC GTC CAG 375  
 101 V T M L Q N I S D N W L G G A F I C K M V P F V Q 125  
 376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 450  
 126 S T A V V T E I L T M T C I A V E R H Q G L V H P 150  
 451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GCA GTC ATC 525  
 151 F K M K W Q Y T N R R A F T M L G V V W L V A V I 175  
 526 GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA ATT GAC TTC CTA ATT GAA AAG GAA CAC ATC TGC 600  
 176 V G S P M W H V Q Q L E I K Y D F L Y E K E H I C 200  
 401 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTC ATC CTC CTC CTG 675  
 201 C L E E W T S P V H Q K I Y T T F I L V I L F L L 225  
 676 CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT ATT GAA ATT TGG ATA AAG AAA AGA GTT GGG GAT GGT 750  
 226 P L M V M L I L Y S K I G Y E L W I K K R V G D G 250  
 751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAG AAA CGA GGT GTC ATT ATG ATG 825  
 251 S V L R T I H G K E M S K I A R K K R A V I M M 275  
 826 GTG ACA GTG GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT ATT GAA TAC AGT AAT 900  
 276 V T V A L F A V C W A P F H V V H M M I E Y S N 300

901 TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC 975  
301 F E K E Y D D V T R I K M I F A I V Q I I G F S N S 325

976 ATC TGT AAT CCC ATT GTC TAT GCA TTT ATG AAT GAA AAC TTC AAA AAA AAT GTT TTG TCT GCA GTT TGT TAT TGC 1050  
326 I C N P I V Y A F M N E N F K N V L S A V C Y C 350

1051 ATA GTA AAT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA ATT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 1125  
351 I V N K T F S P A Q R H G N S G I T M M R K K A K 375

1126 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG 1200  
376 F S L R E N P V E E T K G E A F S D G N I E V K L 400

1201 TGT GAA CAG ACA GAG AAG AAA AAG CTC AAA CGA CAT CTC TCT GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 1275  
401 C E Q T E E K K L K R H L A L F R S E L A E N S 425

1276 CCT TTA GAC AGT GGG CAT TAA 1296  
426 P L D S G H \* 432

## Exhibit 12

### 3' RACE primers

## BAYER CORPORATION

3' RACE

SUBJECT

1	
2	
3	Translated Sequence
4	
5	Range: 1 to 161
6	
7	10 20 30 40 50
8	AGTGACTCATGCCCTGGCCT TTTGGAAATGCTCTGGTGTCTACGT TCACATGAGTAGCGGGACCGCGAGAAACCGTTACGAGACCAAGATGCA S V L I A L A L F G N A L V F Y V >
9	TRANSLATION OF GA1.TXT [A] →
10	60 70 80 90 100
11	→ Nested 6A1 GETGACCGCAGCAAGGCCATGGCACCCTCACCAACATCTTATCTGCT CCACTGGCGTCGTTCCGGTACCGTGGCAGTGGTGTAGAAATAGACGA V T R S K A M R T V T N I F I C >
12	TRANSLATION OF GA1.TXT [A] →
13	
14	110 120 130 140 150
15	CCTTGGCGCTCAGTGACCTGCTCATCACCTTCTGCATTCCCGTCACC GGAACCGCGAGTCACTGGACGAGTAGTGGAAAGAACGTAAGGGCAGTGG S L A L S D L L I T F F C I P V T >
16	TRANSLATION OF GA1.TXT [A] →
17	
18	160
19	ATGAAGCCGAA
20	TAATTGGCTT
21	M K P X >
22	41 22 188 167 53.9 78.0 3.5 56.7 60.4 56.8 48.1 48.1 -3.6 -8.3
23	CCTTGGCGCTCAGTGACCTGCTCATCACCTTCTGCATTCCCGTCACC 27 -43.6 -199.5 -515.1 + CCTCTCTAAAGACTACTATAGGGC 27 -43.0 -205.0 -536.4
24	GA1-F41 (Brian Paesemann 1/19/05)
25	
26	32 74 188 115 52.2 75.4 1.7 54.9 58.6 56.8 48.0 48.1 -4.4 -8.3
27	CCACCTCACCAACATCTTATCTG 25 -40.2 -182.9 -471.0 +
28	GA1-F32 (Brian Paesemann 1/19/05)
29	
30	
31	
32	
33	
34	

SIGNED BY

*Spree*

DATE

WITNESSED AND UNDERSTOOD BY

*Susan Miller*

DATE

CROSS REFERENCES.

## BAYER CORPORATION

SUBJECT

Touch Down PCR for GAT RACE

(15)	5 $\mu$ l cDNA template (Heart)	(Brain)	1
(08)	36 $\mu$ l H <sub>2</sub> O		2
(15)	5 $\mu$ l 10 $\times$ cDNA Buffer		3
(3)	1 $\mu$ l dNTP Mix (10 $\mu$ M)		4
(3)	1 $\mu$ l Ado cDNA polymer mix (50X)		5
	43 $\mu$ l Final	+ 3 $\mu$ l AP1	6
	Program 1 (preferred; use if GSP T <sub>m</sub> > 70°C):		7
	PE DNA Thermal Cycler		8
Heart	1 B126		9
	2 F32		10
	3 F41		11
Brain	4 B126		12
	5 F32		13
	6 F41		14
			15
			16
			17
			18
			19
			20
			21
			22
			23
			24
			25
			26
			27
			28
			29
			30
			31
			32
			33
			34

**PRODUCT:** Human Heart  
Marathon-Ready™ cDNA

CATALOG #: 7404-1

CAT #: 9010719

**STORAGE BUFFER:**

- 10 mM Tricine-KOH (pH 9.2)
- 1 mM EDTA

**STORAGE CONDITIONS:**

- 20°C
- Avoid multiple freeze/thaw cycles.

**SHELF LIFE:**

- 1 year from date of receipt under proper storage conditions

**DESCRIPTION:**

Marathon-Ready cDNA is high-quality, double-stranded cDNA which has been ligated to the Marathon™ Adaptor and is ready for use as a template in 5' and 3' Marathon RACE reactions. In many cases, the full-length cDNA can then be obtained by end-to-end amplification or standard cloning. Enough material is provided for 30 50- $\mu$ l Marathon RACE reactions.

**CONCENTRATION:** = 0.1 ng/ $\mu$ l**POLY A<sup>+</sup> RNA SOURCE:**

Normal, whole hearts pooled from 3 male Caucasians, ages 28-47; cause of death: trauma

No further RNA source information is available.

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

## Exhibit 13

3'-RACE #2 is assembled  
from LZLZ11 and LZLZ21

# **BAYER CORPORATION**

**SUBJECT** human GALS project. Full length 5' + 3' ends.

1 New sequence was deposited in the Life Tools  
2 of unknown protein and called 6A1.pep  
3 - forward  
4

~~6A 1- forward~~

~~chart~~

3'Race#2clone(8.27)  
Sequencher™ "gal 3'&5'"

349 AA.

1047 b.p. Long

5'GAI consensus  
atg cag ggc tt aac att acc ccg gag cag ttc tct cgg ctg ctg cgg gac cac aac ctg acg cgg gag cag ttc atc gtc ctg tac cgg ctg cga cgg ctc gtc  
atg cag ggc tt aac att acc ccg gag cag ttc tct cgg ctg ctg cgg gac cac aac ctg acg cgg gag cag ttc atc gtc ctg tac cgg ctg cga cgg ctc gtc  
M Q A L N I T P E Q F S R L L R D H N L T R E Q F I A L Y R L R P L V  
5'GAI consensus  
#106 tac acc cca gag ctg ccg gga cgc gcc aag ctg gcc ctc gtg ctc acc ggc gtg ctc atc ttc gcc ctg ggc ctc ttt ggc aat gtc ctg gtg ttc tac gtc  
tac acc cca gag ctg ccg gga cgc gcc aag ctg gcc ctc gtg ctc acc ggc gtg ctc atc ttc gcc ctg ggc ctc ttt ggc aat gtc ctg gtg ttc tac gtc  
Y T P E L P G R A K L A L V L T G V L I F A L A L F G N A L V F Y V V  
5'GAI consensus  
45\_JZL221 acc cgc agc aag gcc atg cgc acc aac atc ttt atc tgc tcc ttg ggc ctc agt gac ctg ctc atc acc ttc ttc tgc att ccc gtc acc atg  
#211 gc acc gtc acc aac atc ttt atc tgc tcc ttg ggc ctc agt gac ctg ctc atc acc ttc ttc tgc att ccc gtc acc atg ctc cag  
acc cgc agc aag gcc atg cgc acc gtc acc aac atc ttt atc tgc tcc ttg ggc ctc agt gac ctg ctc atc acc ttc ttc tgc att ccc gtc acc atg  
T R S K A M R T V T N I F I C S L A L S D L L I T F F C I P V T M L Q  
45\_JZL221 aac att tcc gac aac tgg tgg ggg ggt gtc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att gtc  
46\_JZL221 #316 gc att gtc  
aac att tcc gac aac tgg ctg ggg ggt gtc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att gtc  
N I S D N W L G G A F I C K M V P F V Q S T A V V T E I L T M T C I A  
45\_JZL221 gtg gaa agg cac cag gga ctt gtg cat cct ttt aaa atg aag tgg caa tac acc aac cga agg gtc atc atg cta ggt gtg gtc tgg ctg gtg gca gtc atc  
46\_JZL221 #421 gtg gaa agg cac cag gga ctt gtg cat cct ttt aaa atg aag tgg caa tac acc aac cga agg gtc atc atg cta ggt gtg gtc tgg ctg gtg gca gtc atc  
gtg gaa agg cac cag gga ctt gtg cat cct ttt aaa atg aag tgg caa tac acc aac cga agg gtc atc atg cta ggt gtg gtc tgg ctg gtg gca gtc atc  
V E R H Q G L V H P F K M K W Q Y T N R R A F T M L G V V W L V A V I  
45\_JZL221 gta gga tca ccc atg tgg cac gtg cca caa ctt gag atc aaa tat gac ttc cta tat gaa aag gaa cac atc tgc tgg tta gaa gag tgg acc agc cct gtg cac  
46\_JZL221 #526 gta gga tca ccc atg tgg cac gtg cca caa ctt gag atc aaa tat gac ttc cta tat gaa aag gaa cac atc tgc tgg tta gaa gag tgg acc agc cct gtg cac  
gta gga tca ccc atg tgg cac gtg cca caa ctt gag atc aaa tat gac ttc cta tat gaa aag gaa cac atc tgc tgg tta gaa gag tgg acc agc cct gtg cac  
V G S P M W H V Q Q L E I K Y D F L Y E K B H I C C L B E W T S P V H  
45\_JZL221 cag aag atc tac acc acc ttc atc ctt gtc atc ctc ttc ctg cct ctt atg gtg atg ctt att ctg tac agt aaa att ggt tat gaa ctt tgg ata aag aaa  
46\_JZL221 #631 cag aag atc tac acc acc ttc atc ctt gtc atc ctc ttc ctg cct ctt atg gtg atg ctt att ctg tac agt aaa att ggt tat gaa ctt tgg ata aag aaa  
cag aag atc tac acc acc ttc atc ctt gtc atc ctc ttc ctg cct ctt atg gtg atg ctt att ctg tac agt aaa att ggt tat gaa ctt tgg ata aag aaa  
Q K I Y T T F I L V I L F L L P L M V M L I L Y S K I G Y E L W I K K  
JZL221 aga gtt ggg gat ggt tca Gtg ctt cGt act att cat gga aaa gaa atg tcc aaa ata Gcc agg aag aag aaa cga gct gtc att atg atg gtg aca gTg gtg gtc  
JZL221 #736 aga gtt ggg gat ggt tca Gtg ctt cGt act att cat gga aaa gaa atg tcc aaa ata Gcc agg aag aag aaa cga gct gtc att atg atg gtg aca gTg gtg gtc  
R V G D G S V L R T I H G K E M S K I A R K K R A V I M M V T V V A  
Ctc ttt gct Gtg tac tgg Gca ctc ttc gat gtt Gtt  
11

etc ttt act atg tgg tgg gaa gaa ttt

ctc ttt act atg tcc tca ccc gca ttt ccc

you did all day atg att tcc get

etc gta cca att att gca ttt tcc tcc

7477 TGG GGG CGG CCC GTC TGA GTC GCA TGG TGA GTC TCG GAT CCC CGG GTC CGG AGC TCG GAT TCA CTG ACC GTC GTH TTA GCG CG

cta gac cta gcc gtc gtt gca gat gca -

L D L P G C C T A T G A G T A T C G A T C C C C G G G T A C C G A G C T C G A A T T C A C T G A C C A T C G A T T T C A G C C

... V S D P R V P S S N S L A V V I C

© 2023, PRACTICE EXAM

## Exhibit 14

Alignment of 3'-RACE #2  
with SEQ ID NO 1 and SEQ  
ID NO 2

1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CCG GAC CAC AAC CTG ACG CGG GAG CAG TTC 75  
 76 ATC GCT CTG TAC CGG CTG CGA CCG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC 150  
 151 ACC GGC GTC CTC ATC TTC GCC CTG GCG CTC TAC GGC AAT GCT CTG GTG TTC TAC GTG GTG ACC CGC AGC AAG GCC 225

3' -RACE #2 5' -

1    [5C ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTC ATC ACC TIC TIC TGC ATT CCC 71  
 226 ATG CTC ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTC ATC ACC TIC TIC TGC ATT CCC 300

72 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG 146  
 301 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG 375

147 TCT ACC GCT GTT GTG ACA GAA AAC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 221  
 376 TCT ACC GCT GTT GTG ACA GAA AAC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 450

222 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TIC ACA ATG CTA GGT GTG GTC TGG CGT GTG GCA GTC ATC 296  
 451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TIC ACA ATG CTA GGT GTG GTC TGG CGT GTG GCA GTC ATC 525

297 GAA GGA TCA CCC ATG TGG CAA CAA CTT GAG ATC AAA TAT GAC TIC CTA TAT GAA AAG GAA CAC ATC TGC 371  
 526 GAA GGA TCA CCC ATG TGG CAC GTC CAA CAA CTT GAG ATC AAA TAT GAC TIC CTA TAT GAA AAG GAA CAC ATC TGC 600

372 TGC TTA GAA GAG ACC CCT GTG CAC CAG AAG ATC TAC ACC ACC TIC ATC CTT GTC ATC CTC TIC CTC CTG 446  
 601 TGC TTA GAA GAG ACC CCT GTG CAC CAG AAG ATC TAC ACC ACC TIC ATC CTT GTC ATC CTC TIC CTC CTG 675

447 CCT CTT ATG GTG ATG CTT ATT CTG TAC ATG AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 521  
 676 CCT CTT ATG GTG ATG CTT ATT CTG TAC ATG AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 750

522 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAA CGA GCT GTC ATT ATG ATG 596  
 751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAA CGA GCT GTC ATT ATG ATG 825

597 GTG ACA GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC ATG ATT 671  
 826 GTG ACA GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC ATG ATT 900

672 TTT GAA AAG GAA TAT GAT GAT GAT GAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GAA TAC ATG 746  
 901 TTT GAA AAG GAA TAT GAT GAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GAA TAC ATG 975

747 ATC TGT AAT CCC ATT GTC ATT GCA TTT ATG AAT GAA AAC TTGGAAAAAAA 807  
 976 ATC TGT AAT CCC ATT GTC ATT GCA TTT ATG AAT GAA AAC TTG AAA AAA ATT GTT TTG TCT GCA GTT TGT ATT TGC 1050

1051 ATA GTA AAT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA ATT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 1125

-3' -RACE #2

1126 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG 1200  
1201 TGT GAA CAG ACA GAG GAG AAA AAG CTC AAA CGA CAT CTC GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 1275  
1276 CCT TTA GAC AGT GGG CAT TAA 1296

1 M	Q	A	L	N	I	T	P	E	Q	F	S	R	L	R	D	H	N	L	T	R	E	Q	F	25		
26 I	A	L	Y	R	L	R	P	L	V	Y	T	P	E	L	P	G	R	A	K	L	A	L	V	L	50	
51 T	G	V	L	I	F	A	L	A	L	F	G	N	A	L	V	F	Y	V	V	T	R	S	K	A	75	
76 M	R	T	V	T	N	I	F	I	C	S	L	A	L	S	D	L	L	I	T	F	F	C	I	P	100	
101 V	T	M	L	Q	N	I	S	D	N	W	L	G	G	A	F	I	C	K	M	V	P	F	V	Q	125	
V	T	M	L	Q	N	I	S	D	N	W	L	G	G	A	F	I	C	K	M	V	P	F	V	Q	150	
126 S	T	A	V	V	T	E	I	L	T	M	T	C	I	A	V	E	R	H	Q	G	L	V	H	P	175	
S	T	A	V	V	T	E	I	L	T	M	T	C	I	A	V	E	R	H	Q	G	L	V	H	P	200	
151 F	K	M	K	W	Q	Y	T	N	R	R	R	A	F	T	M	L	G	V	V	L	V	A	V	I	225	
F	K	M	K	W	Q	Y	T	N	R	R	R	A	F	T	M	L	G	V	V	L	V	A	V	I	250	
176 V	G	S	P	M	W	H	V	Q	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C	275	
V	G	S	P	M	W	H	V	Q	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C	300	
201 C	L	E	W	T	S	P	V	H	Q	K	I	Y	T	T	F	I	L	V	I	L	F	L	L	325		
C	L	E	W	T	S	P	V	H	Q	K	I	Y	T	T	F	I	L	V	I	L	F	L	L	350		
226 P	L	M	V	M	L	I	Y	S	K	I	G	Y	E	L	W	I	K	K	R	V	G	D	G	426 P		
P	L	M	V	M	L	I	Y	S	K	I	G	Y	E	L	W	I	K	K	R	V	G	D	G	426 P		
251 S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	R	A	V	I	M	M	431 C		
S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	R	A	V	I	M	M	431 C		
276 V	T	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	I	E	Y	S	N	376 F		
V	T	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	I	E	Y	S	N	376 F		
301 F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	S	325	
F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	S	325	
326 I	C	N	P	I	V	Y	A	F	M	N	E	N	E	N	E	N	E	K	N	V	L	S	A	V	C	350
I	C	N	P	I	V	Y	A	F	M	N	E	N	E	N	E	N	E	K	N	V	L	S	A	V	C	350
351 I	V	N	K	T	F	S	P	A	Q	R	H	G	N	S	G	I	T	M	M	R	K	K	A	K	401 C	
376 F	S	L	R	E	N	P	V	E	E	T	K	G	E	A	F	S	D	G	N	I	E	V	K	L	401 C	

## Exhibit 15

Alignment of virtual 1036 nucleotide clone with SEQ ID NO 1 and SEQ ID NO 2

-30-

5GA1 5' - GGTGGCCCCGGCTCCGGAGGGCACAGCA -1

ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CGG GAC CAC AAC CTG ACG CGG GAG CAG TTC  
1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CGG GAC CAC AAC CTG ACG CGG GAG CAG TTC

卷之三

ATC GCT CTG TAC CGG CTG CGA CCG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC  
6 ATC GCT CTG TAC CGG CTG CGA CCG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC

卷之三

Z11 5' - ACCGGGCTGCTCATCTTGCCTGCGCTCTGTTGGCAATGCTGTTCTGTTCTGTTACGTGAGCAAGGCC

11 ACC GGC GTG CTC ATC TTC GGC CTC GTC CTC TTT GGC ATT GCT CTG GTG TTC TAC GTC GTG ACC CGC AAG GCC 225

卷之三

ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC

6 ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TGT GCG CTC AGT GAC CTG CTC ACC TTC ACC ATT CCC  
7 AAGCCGAA-3' 5GA1

卷之三

375 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT ATT TGC AAG ATG GTG CCA TTT GTC CAG  
1 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT ATT TGC AAG ATG GTG CCA TTT GTC CAG  
L2L2Z21 5' -

TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT

6 TCT ACC CCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGG ATT CCT

卷之三

1 ITT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTC GCA GTC ATC

卷之三

6 GAA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC  
GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC 600

卷之三

CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT

9 CCI CII AIG GIG CII AII CIG IAC AGI AII AII CII TGG AII AAG AAA AGA GII GCG GAI GII /

-3' LZLZ11

751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCA AGG AAG AAA CGA GCT GTC ATT ATG ATG  
825 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCA AGG AAG AAA CGA GCT GTC ATT ATG ATG

826 GTG ACA GTC GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT AAT  
900 GTG ACA GTC GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT AAT

901 TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC  
975 TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC

-3' LZLZ21

976 ATC TGT AAT CCC ATT GTC TAT GCA TTT ATG AAT GAA AAC TTC GAAAAA.....AAA  
ATC TGT AAT CCC ATT GTC TAT GCA TTT ATG AAT GAA AAC TTC AAA AAA AAT GTT TTG TCT GCA GTT TGT TAT TGC  
1036 1050

1051 ATA GTC ATT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG  
1126 1126 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG  
1200 1201 TGT GAA CAG ACA GAG GAG AAG AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT  
1275 1276 CCT TTA GAC AGT GGG CAT TAA

1296

1	M	Q	A	L	N	I	T	P	E	Q	F	S	R	L	I	R	D	H	N	L	T	R	E	Q	F	25	
26	I	A	L	Y	R	L	R	P	L	V	Y	T	P	E	L	P	G	R	A	K	L	A	L	V	L	50	
51	T	G	V	L	I	F	A	L	A	L	F	G	N	A	L	V	F	Y	V	V	T	R	S	K	A	75	
76	M	R	T	V	T	N	I	F	I	C	S	L	A	L	S	D	I	L	I	T	F	F	C	I	P	100	
M	R	T	V	T	N	I	F	I	C	S	L	A	L	S	D	I	L	I	T	F	F	C	I	P	125		
01	V	T	T	M	L	Q	N	I	S	D	N	W	L	G	G	A	F	I	C	K	M	V	P	F	V	Q	150
26	S	T	A	V	V	T	E	I	L	T	M	T	C	I	A	V	E	R	H	Q	G	L	V	H	P	175	
51	F	K	M	K	W	Q	Y	T	N	R	R	R	A	F	T	M	L	G	V	V	W	L	V	A	V	I	200
F	K	M	K	W	Q	Y	T	N	R	R	R	A	F	T	M	L	G	V	V	W	L	V	A	V	I	225	
76	V	G	S	P	M	W	H	V	Q	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C	250	
V	G	S	P	M	W	H	V	Q	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C	275		
01	C	L	E	W	T	S	P	V	H	Q	K	I	Y	T	T	F	I	L	V	I	L	F	L	L	L	300	
C	L	E	W	T	S	P	V	H	Q	K	I	Y	T	T	F	I	L	V	I	L	F	L	L	L	325		
26	P	L	M	V	M	L	I	L	Y	S	K	I	G	Y	E	L	W	I	K	R	V	G	D	G	350		
P	L	M	V	M	L	I	L	Y	S	K	I	G	Y	E	L	W	I	K	R	V	G	D	G	375			
51	S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	R	A	V	I	M	M	400		
S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	R	A	V	I	M	M	425			
76	T	V	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	M	I	E	Y	S	N	451	
V	T	V	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	M	I	E	Y	S	N	476	
01	F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	S	501	
F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	S	526		
26	I	C	N	P	I	V	Y	A	F	M	N	E	N	F	EKKKKK (no STOP codon)	K	K	N	V	L	S	A	V	C	Y	C	551
I	C	N	P	I	V	Y	A	F	M	N	E	N	F	EKKKKK (no STOP codon)	K	K	N	V	L	S	A	V	C	Y	C	576	
376	F	S	L	R	E	N	P	V	E	E	T	K	G	E	A	F	S	D	G	N	I	E	V	K	L	400	
401	C	E	Q	T	E	E	K	K	L	K	R	H	L	A	L	F	R	S	E	L	A	E	N	S	425		

## Exhibit 16

### Names of IMAGE/Unigene clones

## BAYER CORPORATION

SUBJECT

Image Clones matching 6A1

m	2055532	g4001837	1
m	2055185	g4002759	2
m	2091776	g4187861	3
m			4
m			5
m			6
m			7

## DNA vs EST Homology Search

source
g4001837
GB:g4001837
GB:g4002759

GB:g4187861

g4001837

Hit ID	P-Value	% ident.	Description
GB:g4001837 (Detail)	0	100	tb27a03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA
Feature	Start	Stop	Description
source	1	432	

ls Analysis Results: 28499

[http://lifetools-e.wh.bayer.com/cgi-bin/incyte/LifeTools/2.0/LT\\_Viewer?id=28499](http://lifetools-e.wh.bayer.com/cgi-bin/incyte/LifeTools/2.0/LT_Viewer?id=28499)

GB:g4002759 (Detail)	0	100	tb23d09.x1 NCI_CGAP_Kid12 Homo sapiens cDNA
Feature	Start	Stop	Description
source	1	432	

GB:g4187861 (Detail)	6.2e-43	100	te67e05.x1 SoaresNFLT_GBC_S1 Homo sapiens
Feature	Start	Stop	Description
source	3	127	

Acc. Num.	Image/Unigene TIGR Indices	Insert Length	Read Length	HQSS	Source (Age/Sex)
AI307658	Im:2055532 Hs.181638	1414	432	419	NCI_CGAP_Kid12 library made from kidney (2 pooled tumors (clear cell type))
AI308124	Im:2055185 Hs.181638	1308	432	429	NCI_CGAP_Kid12 library made from kidney (2 pooled tumors (clear cell type))
AI378008	Im:2091776 Hs.181638		404	364	SoaresNFLT_GBC_S1 library made from pooled

EYNOLDS / NILES, MI / SEPT. 85

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

## Exhibit 17

Location of in-frame STOP  
codon in sequence upstream  
of START methionine

## BAYER CORPORATION

SUBJECT

NRY - Like Clone and primers

### DNA Strider™ 1.2 ###

LGZ1.seq -&gt; Genes

DNA sequence 1902 b.p. TGGCCCTCGAGG ... CTGTGTTCCCTTC linear

1 TGGCCCTCGAGGCGCAAGAATTGGCACGGAGGAGGGGGAGGCCAGAGGGGCCAGGACCCCTGGCTGGCGCTCCAGCACCCAGACCGTGGCGGCGCTCG 100  
 101 CCTTAGGAAAGAGCAAGGGAGAACTTATTTGAACCGGAAACATTGGTCACTGAGATCGAGTCCTCCAGTGCTTGGCTTCCGCCTCTTATCG 200  
 201 TGGGTTGATCCCTGAGCTGCTCCCTTCCCGAACCTGGAGCTGGAGCCCTCCCGGGGCTGACTCCAGAGTAGAGGAACCGGGC 300  
 301 CTCGGGCTGGTCCCCCGAAGCCCTCGCTGCCCGAG ATG CGG ATG GCC AGC CAG TAG CCGGGGGTGGCCCCCGC 392  
 1 M R M A S Q \* →  
 393 ATG CGG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CGG GAC AAC CTG ACG CGG GAG CAG 465  
 1 T G V L I F A L A L G N A L V F Y V V T R S K 24  
 466 TTC ATC GCT CTG TAC CCG CTG CGG CTC GTC TAC ACC CCA GAG CTG CGG GGA CGC GCC AAG CTG GCC CTC GTG 540  
 25 F I A L Y R L R P L Y Y P E L P G R A K L A L V 49  
 541 CTC ACC GGC GTG CTC ATC TIC GCC CTG GGC CTC TTT GGC ATAT GCT CTG GTG TIC TAG GTG GTG ACC CGC AGC AAG 615  
 50 L T G V L I F A L A L G N A L V F Y V V T R S K 74  
 616 GCC ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCT GGC CTC ACT GAC CTG CTC ATC ACC TTC TIC TGC ATT 690  
 75 A M R T V T N I F I C S E A L S D L L I T F F C I 99  
 691 CCC GTC ACC ATC CTC CAG AAC ATT TCC GAC AAC TGG CGG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC 765  
 100 P V T M L Q N I S D N W L G G A F I C K M V P F V 124  
 766 CAG TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT 840  
 125 Q S T A V V T E I L T M T C I A V E R H Q G L V H 149  
 841 CCT TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC 915  
 150 P F K M K W Q Y T N R R A F T M L G V V W L V A V 174  
 916 ATC GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TIC CTA TAT GAA AAG GAA CAC ATC 990  
 175 I V G S P M W H V Q Q L E I K Y D F L Y E K E H I 199  
 991 TGC TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTC ATC CTC TIC CTC 1065  
 200 C C L E E W T S P V H Q K I Y T T F I L V I L F L 224  
 1066 CTG CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT 1140  
 225 L P L M V M L I L Y S K I G Y E L W I K K R V G D 249  
 1141 GGT TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GGC AGG AAG AAG AAA CGA GCT GTC ATT ATG 1215  
 250 G S V L R T I H G K E M S K I A R K K R A V I M 274  
 1216 ATG GTG ACA GTG GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTC CAT ATG ATG ATT GAA TAC AGT 1290  
 275 M V T V V A L F A V C W A P F H V V H M M I E Y S 299  
 1291 AAT TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TGC 1365  
 300 N F E K E Y D V A S T I K M I F A I V P I I G F S N 324  
 1366 TCT CCT TTA GAC AGT GGG CAT TAA TTATAACAAATATCTTCATAATTATG CTC TTT AGG TCT GAA CTG GCT GAG ATT 1440  
 325 S I C N P I V Y A F M N E N F K K N V L S A V C Y 349  
 1441 TGC ATA GTA AAT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA AAT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA 1515  
 350 C I V N K T F S P A Q R H G N S G I T M M R K K A 374  
 1516 AAG TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC ACT GAT GAT GGC AAC ATT GAA GTC AAA 1590  
 375 K F S L R E N P V E E T K G E A F S D G N I E V K 399  
 1591 TTG TGT GAA CAG ACA GAG GAG AAA AAG CTC AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG ATT 1665  
 400 L C E Q T E E K K K L R H L A L F R S E L A E N 424  
 1666 TCT CCT TTA GAC AGT GGG CAT TAA TTATAACAAATATCTTCATAATTATG CTC TTT AGG TCT GAA CCC AAG GAG AAA ATT TTT 1750  
 425 S P L D S G H \* M P F R L 6  
 1751 GAGCAAGGTCAAATACTCTTTTATTCTTAAG ATG ATG ACA AGA AGA AAA CAA ATC ATG TTT CCA TTA AAA AAT GAC ACG 1831  
 1 M M T R R K Q I M F P L K N D T 16  
 1832 AGG CTA GTC CAA STG CAG TGA TGT TTACACATTGATCACAAATCATTTAACACATTCTGTTCCCTC 1902  
 17 R L V Q D  
 B 23

SIGNED BY

WITNESSED AND UNDERSTOOD BY

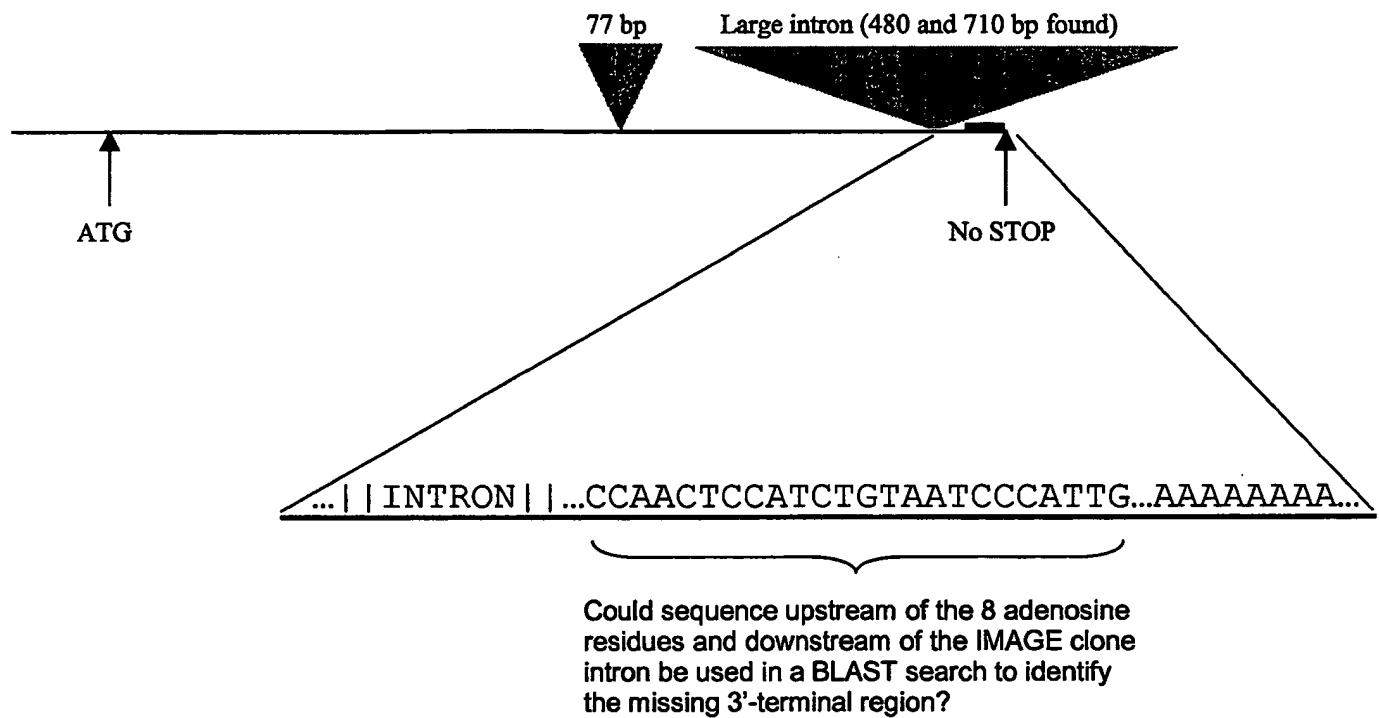
DATE

DATE

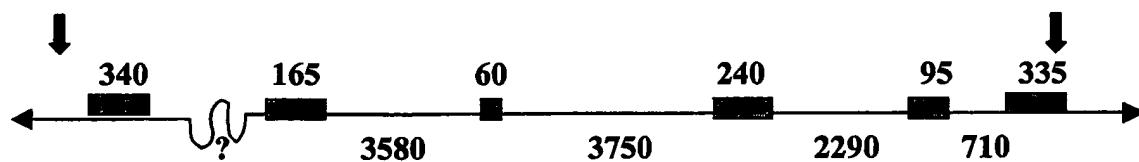
## Exhibit 18

Cloning the 3'-end based on  
IMAGE sequence clues and  
genomic structure of our  
novel GPCR

## Diagram of IMAGE clone structure and BLAST search strategy



## Preliminary genomic structure of novel GPCR



## Exhibit 19

Final electronically  
assembled novel GPCR  
(named LGZ1)

## BAYER CORPORATION

SUBJECT

NRY-like clone and primers

### DNA Strider™ 1.2 ###

LGZ1.seq -&gt; Genes

DNA sequence 1902 b.p. TGGCCCTCGAGG ... CTGTGTCTTC linear

1 TGGCCCTCGAGGCCAAGAACTCGGACAGGAGGAGGGAGCCAGAGGCCAGGACCCCTGGCTGGCTCAGCACCCAGACCGTGGCGCGCTCG 100  
 101 CCTTAGGGAGACCAAGGAAGAACTTTATTAACCGGAGATTTGGTCACTGAGATCGAGTCCTCCAGTGCTTGGCTTCCCCCTCTTATCG 200  
 201 TGGGTTTGAATCCCTGAGCTGCTCTCTTCCCGAACCTGGCTAGAGCCCTCCCGGGCTGACTCCAGTGACAGGAGCGAGGAGCG 300  
 301 CTCCGGCTGGTCCCCCGAACGCCCTGGCTGGCCCGAG ATG CGG ATG GCC AGC CAG TAG [CGGGGGTGGCCCCCGG] SMA 392  
 1 M R M A S Q \* 7  
 392 CTT AAC ATT ACC CGG GAG CAG TTC TCT CGG CTG CTG CGG GAC AAC CTG ACG CGG GAG CAG 465  
 100 P I A L Y R L R P L Y Y T P E Q F S R L L R D H N L T R E Q 24  
 466 TTC ATC GCT CTG TAC CGG CTG CGA CGG CTC GTC TAC ACC CCA GAG CTG CGG GGA CGC GGC AAG CTG GCC CTC GTG 540  
 25 P I A L Y R L R P L Y Y T P E Q F S R L L R D H N L T R E Q 49  
 541 CTC ACC GGC GTG CTC ATC TTC GCC CTG CGG CTC ATT GCT CTG GGC TTC TAA GTG GTG ACC CGC AGC AAG 615  
 50 L T G V L I F A L A E G N A L V E Y V T R S K 74  
 616 GCC ATG CGC ACC GTC ACC AAC ATC TTT ATC TGT TGT GTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT 690  
 75 A M R I T V T N I F I C S E A L S D L L I T F F C I 99  
 691 CCC GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CCG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC 765  
 100 P V T M L Q N I S D N W L G G A F I C K M V P F V 124  
 766 CAG TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT 840  
 125 Q S T A V V T E I L T M T C I A V E R H Q G L V H 149  
 841 CCT TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC 915  
 150 P P K M K W Q Y T N R R A F T M L G V V W L V A V 174  
 916 ATC GTC GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC 990  
 175 I V G S P M W H V Q Q L E I K Y D F L Y E K E H I 199  
 991 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTC CTT GTC ATC CTC TTC CTC 1065  
 200 C C L E E W T S P V H Q K I Y T T F I L V I L P L 224  
 1066 CTG CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT 1140  
 225 L P L M V M L I L Y S K I G Y E L W I K K R V G D 249  
 1141 GGT TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAA CGA GCT GTC ATT ATG 1215  
 250 G S V L R T I H G K E M S K I A R K K R A V I M 274  
 1216 ATG GTG ACA GTG GTG GCT CTC TTT GCT GTG TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT 1290  
 275 M V T V V A L F A V C W A P F H V V H M M I E Y S 299  
 1291 AAT TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TGC AGC 1365  
 300 N F E K E Y D D V D I K M I F A I V W I I G F S N 324  
 1366 CTC TTA GAC AGT GGG CAT TAA TTATAACAATATCTTCTATAATTA ATG CCC TTC AGA TTG TAA CCCAAAGAGAAAATTATTT 1440  
 325 S I C N P I V Y A F M N E N P K K N V L S A V C Y 349  
 1441 TGC ATA GTC AAT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA ATT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA 1515  
 350 C I V N K T F S P A Q R H G N S G I T M M R K K A 374  
 1516 AAG TTT TCC CTC AGA GAG ATT CCA GTG GAG ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA 1590  
 375 K F S L R E N P V E E T K G E A P S D G N I E V K 399  
 1591 TTG TGT GAA CAG ACA GAG GAG AAG AAA AAG CTC AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG ATT 1665  
 400 L C E Q T E E K K K L K R H I A L F R S E L A E N 424  
 1666 TCT CCT TTA GAC AGT GGG CAT TAA TTATAACAATATCTTCTATAATTA ATG CCC TTC AGA TTG TAA CCCAAAGAGAAAATTATTT 1750  
 425 S P L D S G. H. \* M P P R L V 6  
 1751 GAGCAAGGTCAAATACTCTTTTATCTTAAAG ATG ATG ACA AGA AGA AAA CAA ATC ATG TTT CCA TTA AAA ATT GAC ACG 1831  
 1 M M T R R K Q I M F P L K N D T 16  
 1832 AGG CTA GTC CAA GTG CAG TGA TGT TAC ACC ATT GAT CACAATCATTTAACACATTCTGTTCTTC 1902  
 17 R L V Q V Q 23  
 B 23

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

## Exhibit 20

**Alignment of final 300 3'-  
nucleotides against SEQ ID  
NO 1**



## Exhibit 21

Final cloned full-length novel  
GPCR

# **BAYER CORPORATION**

**SUBJECT**

**BAYER CORPORATION**  
Sequencing results of LG21/pETBlue.

1 1. Check if L. Taylor going to clone P.6. receptor.  
2 and when?  
3  
4  
5 2). Clone if sop is ok with one polymorphic

### DNA Strider™ 1.2 ###

### lgz1/pT7Blue#1 sop -> Graphic Map

DNA sequence 1587 b.p. caagcttgcatt ... ccgtcgtttaca linear

432 AA

T<sub>2</sub>  
→

2) Cleoiff & K. Brain is good (same orientation)  
with  $tth \rightarrow ttc$  (Phe) + AA

3) Clone #16 U. Mart is good  
with a/c  $\rightarrow$  att (16) 216 ARS

I cloned using TA-kit  
in pGEMTA3.1 f/f's.

X62 / Barn 3.1 (-)

Wind Shep

لـ

DATE

BASE

**SIGNED BY**

**WITNESSED AND UNDERSTOOD BY**

Terri Witter

## DATE

**DATE**

## **CROSS REFERENCES:**

## BAYER CORPORATION

SUBJECT

Full length cDNA of LGZ1 (NPY-like)

1

in pcDNA3.1 Topo

#1sop/pcDNA3.1Topo  
Sequencher™ "Untitled Project"

HindIII (6)  
KpnI (16)  
SacI (22)  
BamHI (24)  
SpeI (30)  
BstXI (43)  
SmaI (61)

PstI (1560)  
EcorV (1563)  
BstXI (1573)  
NotI (1578)  
XmaIII (1578)  
XhoI (1584)  
XbaI (1590)  
DraII (1596)  
Apal (1600)  
SacII (1603)

ATG (69)

Mapping all cutsites.

Cutters : Apal, BamHI, BstXI, DraII, EcoRI, EcorV, HindIII, KpnI, NotI, PstI, SacI, SacII, SmaI, SpeI, XbaI, XhoI &amp; XmaIII

Non-Cutters : Bsp106 &amp; Sall

start

#1sop/pcDNA3.1Topo  
Sequencher™ "Untitled Project"

PCR of LGZ1 fr. 02\_1Z121 tcc cgg gag cgc aca gca atg cag gcg ctt aac att acc cog gag cag ttc tct egg ctg ctg egg gac cac aac ctg acg cgg gag cag ttc atc gct ctg tac egg ctg cga cgg  
#1 tcc cgg gag cgc aca gca atg cag gcg ctt aac att acc cog gag cag ttc tct egg ctg ctg egg gac cac aac ctg acg cgg gag cag ttc atc gct ctg tac egg ctg cga cgg  
tcc cgg gag cgc aca gca atg cag gcg ctt aac att acc cog gag cag ttc tct egg ctg ctg egg gac cac aac ctg acg cgg gag cag ttc atc gct ctg tac egg ctg cga cgg

Ser Arg Glu Arg Thr Ala MET Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg Asp His Asn Leu Thr Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg Pro

PCR of LGZ1 fr. 02\_1Z121 tcc gtc tac acc cca gag ctg cgg gga cgc gcc aag ctg gcc ctc gtc acc ggc gtc ctc atc ttc gec ctg gec ctc ttt tgc aat gct ctg gtg ttc tac gtg gtg acc cgc  
#118 tcc gtc tac acc cca gag ctg cgg gga cgc gcc aag ctg gcc ctc gtc acc ggc gtc ctc atc ttc gec ctg gec ctc ttt tgc aat gct ctg gtg ttc tac gtg gtg acc cgc  
tcc gtc tac acc cca gag ctg cgg gga cgc gec aag ctg gcc ctc gtc acc ggc gtc ctc atc ttc gec ctg gec ctc ttt tgc aat gct ctg gtg ttc tac gtg gtg acc cgc

Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala Leu Val Phe Tyr Val Val Thr Arg

PCR of LGZ1 fr. 02\_1Z121 agc aag gcc atg cgc acc gtc acc aac atc ttt atc tgc tcc ttg gcg ctc atg acg ctc atc acc ttc ttc tgc att ccc gtc acc atg ctc cag aac att tcc gac aac tgg  
03\_1Z122 agc aag gcc atg cgc acc gtc acc aac atc ttt atc tgc tcc ttg gcg ctc atg acg ctc atc acc ttc ttc tgc att ccc gtc acc atg ctc cag aac att tcc gac aac tgg  
#235 agc aag gcc atg cgc acc gtc acc aac atc ttt atc tgc tcc ttg gcg ctc atg acg ctc atc acc ttc ttc tgc att ccc gtc acc atg ctc cag aac att tcc gac aac tgg

agc aag gcc atg cgc acc aac atc ttt atc tgc tcc ttg gcg ctc atg acg ctc atc acc ttc ttc tgc att ccc gtc acc atg ctc cag aac att tcc gac aac tgg  
Ser Lys Ala MET Arg Thr Val Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe Phe Cys Ile Pro Val Thr MET Leu Gln Asn Ile Ser Asp Asn Trp

PCR of LGZ1 fr. 02\_1Z121 ctg ggg ggt get ttc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att get gtg gaa egg cac gag gga ctt gtg cat cct  
03\_1Z122 ctg ggg ggt get ttc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att get gtg gaa egg cac gag gga ctt gtg cat cct  
#352 ctg ggg ggt get ttc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att get gtg gaa egg cac gag gga ctt gtg cat cct

ctg ggg ggt get ttc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att get gtg gaa egg cac gag gga ctt gtg cat cct  
Leu Gly Gly Ala Phe Ile Cys Lys MET Val Pro Phe Val Gln Ser Thr Ala Val Val Thr MET Thr Cys Ile Ala Val Glu Arg His Gln Gly Leu Val His Pro

WITNESSED AND UNDERSTOOD BY

\_\_\_\_\_  
Lori 2/10/04

DATE

CROSS REFERENCES:



## Exhibit 22

Alignment of LGZ1 clone  
DNA sequence with SEQ ID  
NO 1



919	TTC GAA AGG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC	993	TTC
901	TTC GAA AGG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC	975	TCC
301	F E K E Y D V T I K M I F A I V Q I I G F S N S	325	S
994	ATC TGT ATT CCC ATT GTC TAT GCA TTT ATG AAA AAC TTC AAA AAA ATT GTT TTG TCT GCA GTT TGT ATT TGC	1068	TGC
976	ATC TGT ATT CCC ATT GTC TAT GCA TTT ATG AAA AAC TTC AAA AAA ATT GTT TTG TCT GCA GTT TGT ATT TGC	1050	TGC
326	I C N P I V Y A F M N E N F K K N V L S A V C Y C	350	C
11069	ATA GTA ATT AAA ACC TTC TCT CCA GCA AAA AGG CAT GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG	1143	AAG
11051	ATA GTA ATT AAA ACC TTC TCT CCA GCA AAA AGG CAT GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG	1125	AAG
351	I V N K T F S P A Q R H G N S G I T M M R K A K	375	K
111144	TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG	12118	TTG
111126	TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG	12000	TTG
376	F S L R E N P V E T K G E A F S D G N I E V K L	400	L
112119	TGT GAA CAG ACA GAG GAG AAG AAA CGA CAT CTT CCT CTC TTT AGG TCT GAA CTG GCT GAG ATT TCT	1293	TCT
11201	TGT GAA CAG ACA GAG GAG AAG AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG ATT TCT	1275	TCT
401	C E Q T E E K R K L R H L A L F R S E L A E N S	425	S
11294	CCT TTA GAC AGT GGG CAT TAA TTATAACAAATATCTTCATAAT	1335	
11276	CCT TTA GAC AGT GGG CAT TAA	1296	
426	P L D S G H *	431	

## Exhibit 23

Alignment of LGZ1 clone  
amino acid sequence with  
SEQ ID NO 2



## Exhibit 24

Alignment of assembled  
fragments composing LGZ1  
with SEQ ID NO 2

Clone used for full assembly

1	M	Q	A	L	N	I	T	P	E	Q	F	S	R	L	R	D	H	N	L	T	R	E	Q	F	25	
26	I	A	L	Y	R	L	R	P	L	V	Y	T	P	E	L	P	G	R	A	K	L	A	L	V	L	50
I	A	L	Y	R	L	R	P	L	V	Y	T	P	E	L	P	G	R	A	K	L	A	L	V	L		
51	T	G	V	L	I	F	A	L	A	L	F	G	N	A	L	V	F	Y	V	V	T	R	S	K	A	75
T	G	V	L	I	F	A	L	A	L	F	G	N	A	L	V	F	Y	V	V	T	R	S	K	A		
<i>161 bp fragment - NSAN.seq/GA1</i>																										
76	M	R	T	V	T	N	I	F	I	C	S	L	A	L	S	D	L	I	T	F	F	C	I	P	100	
M	R	T	V	T	N	I	F	I	C	S	L	A	L	S	D	L	I	T	F	F	C	I	P			
<i>161 bp fragment - NSAN.seq/GA1, con't</i>																										
101	V	T	M	L	Q	N	I	S	D	N	W	L	G	G	A	F	I	C	K	N	V	P	F	V	Q	125
V	T	M	L	Q	N	I	S	D	N	W	L	G	G	A	F	I	C	K	M	V	P	F	V	Q		
<i>161 bp fragment - NSAN.seq/GA1, con't</i>																										
126	S	T	A	V	V	T	E	I	L	T	M	T	C	I	A	V	E	R	H	Q	G	L	V	H	P	150
S	T	A	V	V	T	E	I	L	T	M	T	C	I	A	V	E	R	H	Q	G	L	V	H	P		
<i>234 bp fragment - GA2 (con't)</i>																										
151	F	K	M	K	W	Q	Y	T	N	R	R	A	F	T	M	L	G	V	V	W	L	V	A	V	I	175
F	K	M	K	W	Q	Y	T	N	R	R	A	F	T	M	L	G	V	V	W	L	V	A	V	I		
<i>234 bp fragment - GA2 (con't)</i>																										
176	V	G	S	P	M	W	H	V	Q	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C	200
V	G	S	P	M	W	H	V	Q	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C		
<i>234 bp fragment - GA2 (con't)</i>																										
201	C	L	E	W	T	S	P	V	H	Q	K	I	Y	T	F	I	L	V	I	L	F	L	L		225	
C	L	E	W	T	S	P	V	H	Q	K	I	Y	T	F	I	L	V	I	L	F	L	L				
<i>3'RACE #2</i>																										
226	P	L	M	V	M	L	I	L	Y	S	K	I	G	Y	E	L	W	I	K	R	V	G	D	G	250	
P	L	M	V	M	L	I	L	Y	S	K	I	G	Y	E	L	W	I	K	R	V	G	D	G			
<i>3'RACE #2</i>																										
251	S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	R	A	V	I	M	M	275	
S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	R	K	R	V	G	D	G		
<i>3'RACE #2</i>																										
276	V	T	V	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	I	E	Y	S	N	300
V	T	V	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	I	E	Y	S	N		
<i>3'RACE #2</i>																										
301	F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	325	
F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N			
<i>3'RACE #2</i>																										
326	I	C	N	P	I	V	Y	A	F	M	N	E	N	E	K	K	N	V	L	S	A	V	C	Y	350	
I	C	N	P	I	V	Y	A	F	M	N	E	N	E	E	K	K	N	V	L	S	A	V	C	Y		

300 nt 3'-end

351 I V N K T F S P A Q R H G N S G I T M M R K K A K 375  
I V N K T F S P A Q R H G N S G I T M M R K K A K

376 F S L R E N P V E E T K G E A F S D G N I E V K L 400  
F S L R E N P V E E T K G E A F S D G N I E V K L

401 C E Q T E K R L K R H L A L F R S E L A E N S 425  
C E Q T E K R L K R H L A L F R S E L A E N S

426 P L D S G H \* 431  
P L D S G H \*

300 nt 3'-end

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- BLACK BORDERS**
- IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- FADED TEXT OR DRAWING**
- BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- SKEWED/SLANTED IMAGES**
- COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- GRAY SCALE DOCUMENTS**
- LINES OR MARKS ON ORIGINAL DOCUMENT**
- REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- OTHER: \_\_\_\_\_**

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**